

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: November 1, 2004, 18:01:56 ; Search time 85 Seconds
(without alignments)

1187.436 Million cell updates/sec

Title: US-09-690-825-34
Perfect score: 778
Sequence: 1 MGAPFLPAPMOPLKDHRI.....EFETAKVRAIEQLAAMD 142

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_p2n.model -DEV=xlp
-Q=/cgn2_1/USFTO.spool.p/US09690825/funat.0112004.105430.1882/app.query.fasta_1.327
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -INTS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humana0.cdi
-LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09690825.@cgn2_1.105.funat.0112004.105430.1882 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELACK=100 -LONELIG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:
Issued Patents NA:
1: /cgn2_6/prodata/1/ins/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ins/5B_COMB.seq.*
3: /cgn2_6/prodata/1/ins/6A_COMB.seq.*
4: /cgn2_6/prodata/1/ins/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ins/PCUTS_COMB.seq.*
6: /cgn2_6/prodata/1/ins/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	426	3	US-09-283-144-2 6346389 Sequence 1, Appl
2	778	100.0	1619	3	US-09-163-162-1 607709 Sequence 1, Appl
3	778	100.0	1619	3	US-09-286-407-1 Sequence 1, Appl
4	778	100.0	1619	3	US-09-496-694B-97 Sequence 97, Appl
5	778	100.0	1619	3	US-08-448-722A-1 Sequence 1, Appl
6	778	100.0	1619	3	US-08-189-309B-1 Sequence 1, Appl
7	778	100.0	1619	3	US-09-016-434-918 Sequence 918, Appl
8	778	100.0	1619	3	US-09-496-694B-10 Sequence 10, Appl
9	778	100.0	1619	3	US-09-513-599C-2315 Sequence 2315, Appl
10	778	100.0	1619	3	US-08-975-080-35 Sequence 35, Appl
11	778	100.0	1619	3	US-08-630-706-10 Sequence 10, Appl
12	778	100.0	1619	3	US-09-496-694B-3 Sequence 3, Appl

13	246.5	31.7	624	4	US-09-738-946-3	Sequence 3, Appl
14	244.5	31.4	665	4	US-09-270-767-10343	Sequence 10343, A
15	221	28.4	417	3	US-09-283-144-1	Sequence 1, Appl
16	157	20.2	481	4	US-09-270-767-11886	Sequence 11886, A
17	155	19.9	5366	4	US-09-705-872-4	Sequence 4, Appl
18	155	19.9	5302	3	US-08-836-134-1	Sequence 1, Appl
19	155	19.9	5502	4	US-09-493-784-1	Sequence 1, Appl
20	155	19.9	5502	4	US-09-023-655-1459	Sequence 1459, Ap
21	155	19.9	5984	4	US-09-705-872-2	Sequence 2, Appl
22	136.5	17.5	1134	4	US-09-502-528-2	Sequence 2, Appl
23	136.5	17.5	1337	4	US-09-127-928-1	Sequence 1, Appl
24	136.5	17.5	1739	4	US-09-502-528-1	Sequence 1, Appl
25	131	16.8	1559	3	US-09-239-867-1	Sequence 1, Appl
26	131	16.8	1559	4	US-10-024-433-1	Sequence 1, Appl
27	131	16.8	2580	2	US-08-511-485-7	Sequence 7, Appl
28	131	16.8	2580	4	US-09-201-936-7	Sequence 7, Appl
29	131	16.8	2580	4	US-09-011-356-7	Sequence 7, Appl
30	131	16.8	2580	4	US-09-672-717-222	Sequence 222, App
31	131	16.8	2580	4	US-09-201-932-7	Sequence 7, Appl
32	131	16.8	2589	5	PCT-US96-749-1	Sequence 1, Appl
33	131	16.8	2589	3	US-09-205-204-1	Sequence 1, Appl
34	131	16.8	3532	2	US-09-212-971-7	Sequence 7, Appl
35	131	16.8	3732	3	US-08-800-929A-7	Sequence 7, Appl
36	131	16.8	3732	3	US-09-617-053A-7	Sequence 7, Appl
37	131	16.8	711	3	US-08-121-978-3	Sequence 3, Appl
38	130	16.7	711	3	US-09-332-319-3	Sequence 3, Appl
39	130	16.7	711	3	US-09-248-786A-1277	Sequence 1277, Ap
40	130	16.7	1929	4	US-08-511-485-9	Sequence 9, Appl
41	129.5	16.6	2100	2	US-09-201-936-9	Sequence 9, Appl
42	129.5	16.6	2100	4	US-09-011-356-9	Sequence 9, Appl
43	129.5	16.6	2100	4	US-09-672-717-224	Sequence 224, App
44	129.5	16.6	2100	4	US-09-201-932-9	Sequence 9, Appl
45	129.5	16.6	2100	4	US-09-201-932-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-283-144-2
; Sequence 2, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; EARLIER FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21860
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of open reading frame encoding
US-09-283-144-2
Alignment Scores:
Pred. No.: 3,556-93
Score: 778.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 426
Matches: 142
Mismatch: 0
Indels: 0

DB: 3 Gaps: 0
US-09-690-825-34 (1-142) x US-09-283-144-2 (1-426)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 1 ATGGGTGCCCCGAGCTGGCCCCCTGGCCGAGCCCTTTCTCAAGAGCAACCCGATCTCT 60
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 61 ACATTCAAGAACTGGCCCTTTCTTGAAGGCTGCCCTTGCACCCGAGCGGATGGCCGAG 120
QY 41 AlaGlyPheIleHisCysProThrGlnAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 121 GCTGGCTTCATCCACTGGCCCACTGAGAACGAGCAAGCTTGGCCGAGCTTCTTCTGC 180
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisIleLysHis 80
DB 181 TTCAAGAGCTGGAAGCTGGAGCCAGATGACACCCCAAGAGCAATTAAGCAT 240
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
DB 241 TCGTCCGGTGGCTTTCCTTCTTCTGTCAGAGAGCAGTTTGAAGATTAACTTGGTGA 300
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 301 TTTTGAAGCTGAGCAAGAGAAAGCCAGAAATTCAAAGAGAAACCAATTAAG 360
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaIle 140
DB 361 AAGAAAGATTGAGGAAACTGCGAAGAAAGTGGCCCTGCTCCATCGAGCAGCTGGCTGC 420
QY 141 MetAsp 142
DB 421 ATGGAT 426
RESULT 2
US-09-163-162-1
; Sequence 1, Application US/09163162
; Patent No. 6077709
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Coswert, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: RUS-0008
; CURRENT APPLICATION NUMBER: US/09/163,162
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(478)
US-09-163-162-1
Alignment Scores:
Pred. No.: 2,65e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-690-825-34 (1-142) x US-09-163-162-1 (1-1619)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCGAGCTGGCCCCCTGGCCGAGCCCTTTCTCAAGAGCAACCCGATCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTTCTTGAAGGCTGCCCTTGCACCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGlnAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GCTGGCTTCATCCACTGGCCCACTGAGAACGAGCAAGCTTGGCCGAGCTTCTTCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisIleLysHis 80
DB 230 TTCAAGAGCTGGAAGCTGGAGCCAGATGACGCCCAATTAAGAGCAATTAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
DB 290 TCGTCCGGTGGCTTTCCTTCTTCTGTCAGAGAGCAGTTTGAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 350 TTTTGAAGCTGAGCAAGAGAAAGCCAGAAATTCAAAGAGAAACCAATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaIle 140
DB 410 AAGAAAGATTGAGGAAACTGCGAAGAAAGTGGCCCTGCTCCATCGAGCAGCTGGCTGC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475
RESULT 3
US-09-286-407-1
; Sequence 1, Application US/09286407A
; Patent No. 6165788
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Coswert, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0345
; CURRENT APPLICATION NUMBER: US/09/286,407A
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 1
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(478)
US-09-286-407-1
Alignment Scores:
Pred. No.: 2,65e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-690-825-34 (1-142) x US-09-286-407-1 (1-1619)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCGAGCTGGCCCCCTGGCCGAGCCCTTTCTCAAGAGCAACCCGATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTTCTTGAAGGCTGCCCTTGCACCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGlnAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GCTGGCTTCATCCACTGGCCCACTGAGAACGAGCAAGCTTGGCCGAGCTTCTTCTGC 229

QY 61 PheLeuSGluLeuSGluGluYTrpGluProAspAspProIleGluGluHisIleSlySlySHS 80
DB 230 TTCACAGAGCTGGACAGCTGGAGCGAGATGACGACCCCATGAGAAACNTAAAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValIleSlySGluPheGluGluLeuThrLeuGluGlu 100
DB 290 TCGTCCGCTGGCTTCTCTTCTGTCACAGACGATTTGAAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaIleSlySlySlyIleAlaIleSlyGluThrAsnSlyS 120
DB 350 TTTTGAACCTGACAGAGAAAGCCCAAGAAATTCAGAAAGGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluGluThrAlaIleSlySlyValArgArgAlaIleGluGluLeuAla 140
DB 410 AAGAAAGATTGAGAAAGAACTGGAGAAAGTGGCCCTGCTCCATCGACGCTGGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGAT 475
RESULT 4
US-09-496-694B-97
/ Sequence 97, Application US/09496694B
/ Patent No. 6335194
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ APPLICANT: Elizabeth J. Ackermann
/ APPLICANT: Eric B. Swayze
/ APPLICANT: Lex M. Cowsett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
/ FILE REFERENCE: ISPH-0439
/ CURRENT APPLICATION NUMBER: US/09/496,694B
/ PRIOR FILING DATE: 2000-02-02
/ PRIOR APPLICATION NUMBER: 09/286,407
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: 09/163,162
/ PRIOR FILING DATE: 1998-09-29
/ NUMBER OF SEQ ID NOS: 249
/ SEQ ID NO 97
/ LENGTH: 1619
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-496-694B-97
Alignment Scores:
Pred. No.: 2,65e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-690-825-34 (1-142) x US-09-496-694B-97 (1-1619)
QY 1 MetGlyAlaProThrLeuProProAlaIleTrpGluProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGGTCCCGACGCTGGCCCTGCTGGACCCCTTCTCAAGACCAACCCGACATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGluCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAGAACTGGCCCTTCTGGAGGCTGGCGCTGCACCCCGAGGCGAGTGGCGAG 169
QY 41 AlAGlyPheIleHisCysProThrGluArgGluProAspLeuAlaGluCysPhePheCys 60
DB 170 GCTGGCTTCACTCACTCCCTGACAGAGAGCCGACACTTGGCCCACTGTTCTTCTG 229
QY 61 PheLysGluLeuGluGluYTrpGluProAspAspAspProIleGluGluHisIleSlySlySHS 80
DB 230 TTCACAGAGCTGGACAGCTGGAGCGAGATGACGACCCCATTAAGAACTTAAGAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValIleSlySGluPheGluGluLeuThrLeuGluGlu 100
DB 290 TCGTCCGCTGGCTTCTCTTCTGTCACAGACGATTTGAAAGATTAACTTGGTGA 349

QY 101 PheLeuLysLeuAspArgGluArgAlaIleSlySlySlyIleAlaIleSlyGluThrAsnSlyS 120
DB 350 TTTTGAACCTGACAGAGAAAGCCCAAGAAATTCAGAAAGGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluGluThrAlaIleSlySlyValArgArgAlaIleGluGluLeuAla 140
DB 410 AAGAAAGATTGAGAAAGAACTGGAGAAAGTGGCCCTGCTCCATCGACGCTGGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGAT 475
RESULT 5
US-08-448-722A-1/c
/ Sequence 1, Application US/08448722A
/ Patent No. 6072028
/ GENERAL INFORMATION:
/ APPLICANT: Altieri, Dario C.
/ TITLE OF INVENTION: NO. 6072028e1 Cell Surface Receptor, Antibody
/ TITLE OF INVENTION: Compositions, and Methods of Using Same
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Office of Patent Counsel, The Scripps
/ ADDRESS: Research Institute
/ STREET: 10550 No. 6072028th Torrey Pines Road, TPC-8
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: US
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/448,722A
/ FILING DATE: 25-MAY-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/189,309
/ FILING DATE: 28-JAN-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: 233.1 Div1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 784-2937
/ TELEFAX: (619) 784-9399
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1165 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 37..1047
US-08-448-722A-1
Alignment Scores:
Pred. No.: 1,42e-88 Length: 1165
Score: 748.00 Matches: 140
Percent Similarity: 99.30% Conservative: 1
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 96.14% Indels: 1
DB: 3 Gaps: 0
US-09-690-825-34 (1-142) x US-08-448-722A-1 (1-1165)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
DB 1114 ATGGATGCCCCGAGCTGCCCCCTGCTGGAGGCCCTTTCTCAAGAGCCACCCGATCTCT 1055
QY 21 ThrPheLysAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 1054 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCC -TGCACCCCGAGGCGGATGGCCGAG 996
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 995 GCTGGCTTCATCCACTGCCCCACGAGACGACACTTGGCCGATGTTCTTCTTCTGCG 936
QY PheLeuGluLeuGluGlyTTPGluProAspAspProIleGluHisIleLysGluThrAsnLys 80
DB 935 TTCAAGAGCTGAGAGCTGGAGCCGACATGACACCCCTAGAGAACTATAAAGCAT 876
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGlyGlu 100
DB 875 TCGTCCGGTTCGCTTCTTCTGTCAGAGACGATTTAAGATTAACTTGGTGA 816
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 815 TTTTGAACCTGACAGAGAAAGCCAGAACAAATTGCAAGAAACCAATTAAG 756
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140
DB 755 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGCGCTGCATCGAGCTGGCTCG 696
QY 141 MetAsp 142
DB 695 ATGGAT 690

RESULT 6

US-08-189-309B-1/c

Sequence 1, Application US/08189309B

Patent No. 6238875

GENERAL INFORMATION:

APPLICANT: Alterm, Dario C.

TITLE OF INVENTION: Diagnostic Methods Useful in the Characterization of

NUMBER OF SEQUENCES: 5 Lymphoproliferative Disease Characterized by Increased EPR-1

CORRESPONDENCE ADDRESS:

ADDRESSER: Office of Patent Counsel, The Scripps

STREET: 10550 No. 6238875th Torrey Pines Road, TPC-8

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/189,309B

FILING DATE: 28-JAN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,897

FILING DATE: 10-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/667,957

FILING DATE: 12-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: 233.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9398

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 37..1047
US-08-189-309B-1

Alignment Scores:
Pred. No.: 1,42e-88 Length: 1165
Score: 748.00 Matches: 140
Percent Similarity: 99.30% Conservative: 1
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 96.14% Indels: 1
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-189-309B-1 (1-1165)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
DB 1114 ATGGATGCCCCGAGCTGCCCCCTGCTGGAGGCCCTTTCTCAAGAGCCACCCGATCTCT 1055
QY 21 ThrPheLysAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 1054 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCC -TGCACCCCGAGGCGGATGGCCGAG 996
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 995 GCTGGCTTCATCCACTGCCCCACGAGACGACACTTGGCCGATGTTCTTCTTCTGCG 936
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluHisIleLysGluThrAsnLys 80
DB 935 TTCAAGAGCTGAGAGCTGGAGCCGACATGACACCCCTAGAGAACTATAAAGCAT 876
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGlyGlu 100
DB 875 TCGTCCGGTTCGCTTCTTCTGTCAGAGACGATTTAAGATTAACTTGGTGA 816
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 815 TTTTGAACCTGACAGAGAAAGCCAGAACAAATTGCAAGAAACCAATTAAG 756
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140
DB 755 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGCGCTGCATCGAGCTGGCTCG 696
QY 141 MetAsp 142
DB 695 ATGGAT 690

RESULT 7

US-09-016-434-918

Sequence 918, Application US/09016434

Patent No. 650938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSER: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 918:
SEQUENCE CHARACTERISTICS:
LENGTH: 740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRA1TUT01
CLONE: 752848
US-09-016-434-918

Alignment Scores:
Pred. No.: 2,556-85 Length: 740
Score: 721.00 Matches: 135
Percent Similarity: 95.74% Conservative: 0
Best Local Similarity: 95.74% Mismatches: 6
Query Match: 92.67% Indels: 1
Gaps: 0

US-09-690-825-34 (1-142) x US-09-016-434-918 (1-740)

QY 2 G1YAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSerThr 21
Db 22 GGGGCGCNCNGCTGGCCACT-GCCTGGCCTCCCTTCTCAAGACCGCATCTCTACA 80

QY 22 PheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGluAla 41
Db 81 TTCAAGAACTGGCCCTCTTGGAGGGCTGGCTGCACCCCGAGGAGATGGCGGAGCT 140

QY 42 G1YPheIleHisCysProThrGluAsnGluProAspLeuLysGlnCysPhePheCysPhe 61
Db 141 GGCTTCATCCACTGCCCACTGAMAAAGACGACACTGGCCCAAGTCTTCTCTGCTTC 200

QY 62 LysGlnLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysSer 81
Db 201 AAGGAGCTGGAAGGCTGGAGCCGATGACGACCCCTAAGAGAACTAAAGCAATTCG 260

QY 82 SerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGluGluPhe 101
Db 261 TCCGCTTGGCTTCTCTTCTTCTGTCAGAGACGATGAGAAATTAACCTTGGGAATTT 320

QY 102 LeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 121
Db 321 TTGAAACTGGACAGAGAAAGCCCAAGAACAAATTCAAGAGAAACCAACATTAAGAAG 380

QY 122 LysGlnPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaMet 141
Db 381 AAAAGATTTGAGAACTGGAGAAAGTGCGCGCTCCATCGAGCGCTGGCTGCCATG 440

QY 142 Asp 142
Db 441 GAT 443

RESULT 8
US-09-496-694B-10

Sequence 10, Application US/09496694B
Patent No. 6335194
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric B. Swartz
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 10
LENGTH: 955
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (109)...(531)
US-09-496-694B-10

Alignment Scores:
Pred. No.: 3,956-77 Length: 955
Score: 660.00 Matches: 118
Percent Similarity: 92.66% Conservative: 12
Best Local Similarity: 84.29% Mismatches: 10
Query Match: 84.83% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-10 (1-955)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
Db 109 ATGGAGCTCCGGCCCTCCCAAGATCGGAGCTGTACTCTCAAGAACTACCGCATCGCC 168

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 169 ACCTTCAGAACTGGCCCTCTCTGGAGGACTGGCGCTGCACCCAGAGCGAATGGCGAG 228

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuLysGlnCysPhePheCys 60
Db 229 GCTGGCTTCATCCACTGCCCTTACCGAGAACGAGCTGATTTGGCCAGTCTTTTCTGC 288

QY 61 PheLysGlnLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysSer 80
Db 289 TTTAAGAAATTTGAAGAGCTGGGAACCGATGACCAACCGATAGAGACATAGAAAGAC 348

QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGluGlu 100
Db 349 TCCCTGCTGGCGCTTCTCTCTCAAGAGAGATGAGAACTAACCGTCACTAA 408

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 409 TTCTTGAACCTGGACAGACAGAGCCCAAGAACAAATTGCAAGAGAACCAACACACAG 468

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140
Db 469 CAAAAGATTGAGAGACACTGCAAGAGCTACCCGCTCAGTCAATTGACAGCTGCTGCC 528

RESULT 9
US-09-513-999C-2315
Sequence 2315, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ducaslet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

FILE REFERENCE: 59. US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2315
LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 52..399
FEATURE:
NAME/KEY: misc_feature
LOCATION: 32
OTHER INFORMATION: k=g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 279
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 280
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 318
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 342
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: UNSURE
LOCATION: 77
OTHER INFORMATION: Xaa=asp or His
US-09-513-999C-2315

Alignment Scores:
Pred. No.: 2,47e-75 Length: 399
Score: 642.00 Matches: 115
Percent Similarity: 99.14% Conservative: 0
Best Local Similarity: 99.14% Mismatches: 1
Query Match: 82.52% Indels: 0
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-513-999C-2315 (1-399)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuYsaPhtsArgIleSer 20
DB 52 ATGGGTGCCCCGAGCTTGCCCCCTGCGCAGCCCTTTCTCAAGACCCACCCATCTCT 111
QY 21 ThrPheYsaAntpProPheLeuGluGlyCysAlaCysThrProGluuArgMetAlaGlu 40
DB 112 ACATTCAAGAACTGGCCCTCTTGAGAGGCTGCGCCCTGCACCCCGAGCGAGTGGCCGAG 171
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuIaGlnCysPhePheCys 60
DB 172 GCTGGCTTCATCCACTGCCCCCACTGAGAACGACCACTTGGCCCACTTTCTTCTCTG 231
QY 61 PheIleGluLeuGluGlyTrpGluProAspAspProIleGluuHisIleYsHis 80
DB 232 TTCAAGAGAGCTGGAAGGCTGGGAGCCAGATGACGACCCCATAGAGGARSYTAAGACAT 291
QY 81 SerGergIYcysAlaPheLeuSerValIleYsIleGlnPheGluLeuThrIleuGluYglu 100
DB 292 TCGTCGGGTGGCGCTTCTCTTCTGTSAAAGAGAGATTGAGAGATTAACTTGGTGA 351
QY 101 PheLeuYsLeuAspArgIuArgAlaIeYsAsnYsIleAlaYsGlu 116
DB 352 TTTTGAAGTGGACAGAAAGAGCCAGAACAAATTGCAAGGAA 399

RESULT 10
US-08-975-080-35
Sequence 35, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Allier, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
NUMBER OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1900 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
FAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-975-080-35

Alignment Scores:
Pred. No.: 8.89e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 3 Gaps: 1

US-09-690-825-34 (1-142) x US-08-975-080-35 (1-14796)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuYsaPhtsArgIleSer 20
DB 2811 ATGGGTGCCCCGAGCTTGCCCCCTGCGCAGCCCTTTCTCAAGACCCACCCATCTCT 2870
QY 21 ThrPheYsaAntpProPheLeuGluGlyCysAlaCysThrProGluuArg- 37
DB 2871 ACATTCAAGAACTGGCCCTCTTGAGAGGCTGCGCCCTTGACACCCCGAGCGGTAGACTG 2930
QY 37 ----- 37
DB 2931 CCCGGCTCTGAGGTCGCCACCGCCGCTTGCTGCTGCTGAGGAGGACACTGTGAC 2990
QY 37 ----- 37
DB 2991 TGGGCTCGGAGGATCAAGCCGCTTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 3050
QY 37 ----- 37
DB 3051 GGCTGGCCCTTGAGTCCAGGCGGCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3110

```

QY 37 ----- 37
Db 3111 TGTGGCTGGGCTTCGGGGCTTCGGGCTGCACGCTCCAGCTGCTGTCTCCCTTG 3170

QY 38 ---MetaIaGluAaGlyPheIIeHisCysProThrGluAsnGluProAspLeuAaGln 56
Db 3171 CAGATGGCCCGAGGCTGGCTTCATCCACTGCCCCACAGAGACGAGCAGACTTGGCCCGAG 3230

QY 57 CysPhePheCysPheLysGluLeuGluGlyTyrGluProAspAspAspProile 74
Db 3231 TGTTCCTTCCTTCCTTCAGAGAGCTGGAGAGCTGGAGAGCCAGATGACAGCCCATG 3284

RESULT 11
US-09-630-706-10
; Sequence 10, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630,706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 10
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-630-706-10

Alignment Scores:
Pred. No.: 8,896-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 3 Gaps: 1

US-09-690-825-34 (1-142) x US-09-630-706-10 (1-14796)
QY 1 MetGlyAlaProThrLeuProProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCCGAGCGTTGGCCCTGCTGGCAGCCCTTTCTCAAGAGACCGCATCTCT 2870

QY 21 ThrPheLysAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArg 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCGCTGCACCCCGAGCGGGTGAAGACTG 2930

QY 37 ----- 37
Db 2931 CCGGCTCTCTGGGGTCCCGCAGCCCGCTTGCCTGTCCCTAGAGAGCCACTGTGAC 2990

QY 37 ----- 37
Db 2991 TGGGCTCTGGGGGATACAGCCGCTTCCTCCCGCTGTCTCCCGAGAGGCCACTGT 3050

QY 37 ----- 37
Db 3051 GAGTGGGCCCTTGGGTCAAGCGCGGCTCCCTCCCTGTGTGTCATCGAGGCTT 3110

QY 37 ----- 37
Db 3111 TGTGGCTGGGCTTCGGGGTTCGGGGCTGCACGTCACATCAAGAGCTGTCTCTGCTTG 3170

```

```

QY 38 ---MetaIaGluAaGlyPheIIeHisCysProThrGluAsnGluProAspLeuAaGln 56
Db 3171 CAGATGGCCCGAGGCTGGCTTCATCCACTGCCCCACAGAGACGAGCAGACTTGGCCCGAG 3230

QY 57 CysPhePheCysPheLysGluLeuGluGlyTyrGluProAspAspAspProile 74
Db 3231 TGTTCCTTCCTTCCTTCAGAGAGCTGGAGAGCTGGAGAGCCAGATGACAGCCCATG 3284

RESULT 12
US-09-496-694B-3
; Sequence 3, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-496-694B-3

Alignment Scores:
Pred. No.: 8,896-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 3 Gaps: 1

US-09-690-825-34 (1-142) x US-09-496-694B-3 (1-14796)
QY 1 MetGlyAlaProThrLeuProProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCCGAGCGTTGGCCCTGCTGGCAGCCCTTTCTCAAGAGACCGCATCTCT 2870

QY 21 ThrPheLysAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArg 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCGCTGCACCCCGAGCGGGTGAAGACTG 2930

QY 37 ----- 37
Db 2931 CCGGCTCTCTGGGGTCCCGCAGCCCGCTTGCCTGTCCCTAGAGAGCCACTGTGAC 2990

QY 37 ----- 37
Db 2991 TGGGCTCTGGGGGATACAGCCGCTTCCTCCCGCTGTCTCCCGAGAGGCCACTGT 3050

QY 37 ----- 37
Db 3051 GAGTGGGCCCTTGGGTCAAGCGCGGCTCCCTCCCTGTGTGTCATCGAGGCTT 3110

QY 37 ----- 37
Db 3111 TGTGGCTGGGCTTCGGGGTTCGGGGCTGCACGTCACATCAAGAGCTGTCTCTGCTTG 3170

```

Db 3111 TGTGGCTGGGCTCGGGGTTCCGGGCTGCCACGTCACCTCAGAGCTGTGTCGCTTG 3170
Qy 38 ---MetlaagluAaGlyPheIleHisCysProThrGluSngluPProAblLeuAlaGln 56
Db 3171 CAGATGGCCGAGGCTGCTTCATCCACTGCCCTCAGAACGAGCCGACCTGGCCGAG 3230
Qy 57 CysPhePheCysPheLysGluLeuGluGlyTrrpGluProAspAspPhe 74
Db 3231 TGTTCCTTCCTTCCTTCAGAGAGCTGGAAAGCTGGAGCCAGCATGAGCCACCA 3284

RESULT 13
US-09-738-946-3
; Sequence 3, Application US/09738946
; Patent No. 6579701
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCER
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: EX00-043C
; CURRENT APPLICATION NUMBER: US/09/738,946
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/170,832
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/170,838
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/178,580
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/185,879
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/185,880
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/186,150
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/189,701
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent version 3.0
; SEQ ID NO 3
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-738-946-3

Alignment Scores:
Pred. No.: 5,01e-23 Length: 624
Score: 246.50 Matches: 48
Percent Similarity: 57.14% Conservative: 20
Best Local Similarity: 40.34% Mismatches: 50
Query Match: 31.68% Indels: 1
Gaps: 4

US-09-690-825-34 (1-142) x US-09-738-946-3 (1-624)
Qy 14 LeuLysAspHisArgIleSerThrPheLysAsnTrrpProPheLeuGluGlyCysAlaCys 33
Db 139 CTGGAACAGCATCGCGGAGAGCTACAGAGTTGGCCCTTCGAGAGCCGATCTCG 198
Qy 34 ThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluSngluPProAsp 53
Db 199 AGCATTTGGAAGAGCGCCGAGCGCGGATTCATTGACCGGCGACCAAGCGGAAAAAGCAG 258
Qy 54 LeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrrpGluProAspAspPhe 73
Db 259 ACTGCCACTTGTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 318
Qy 74 IleGluGluHisLysLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPhe 93
Db 319 TGGAAAGAGCAGCGGAAACATGACCCCAATGCGAGTTCCCAAGCTATGTCCTCCGAA 378
Qy 94 GluGluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
Db 379 AGGAATTAAACCGATACCAATTTCCTGGAATTCCTTGGAACCGTCTTAAGGACAGATA 438

Qy 114 AlaLysGluThrAsnAsnLysLysLysGluPhe---GluGluThrAlaLysLysVal 131
Db 439 GAGAAAGCTGCAAAAGCTTCAATCGAGCTTCCTTCGAGAGATGAGAGCGCTTA 495

RESULT 14
US-09-270-767-10343
; Sequence 10343, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 10343
; LENGTH: 665
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10343

Alignment Scores:
Pred. No.: 1,01e-22 Length: 665
Score: 244.50 Matches: 48
Percent Similarity: 56.30% Conservative: 19
Best Local Similarity: 40.34% Mismatches: 51
Query Match: 31.43% Indels: 1
Gaps: 4

US-09-690-825-34 (1-142) x US-09-270-767-10343 (1-665)
Qy 14 LeuLysAspHisArgIleSerThrPheLysAsnTrrpProPheLeuGluGlyCysAlaCys 33
Db 182 CTGGAACAGCATCGCGGAGAGCTACAGAGTTGGCCCTTCGAGAGCCGATCTCG 241
Qy 34 ThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluSngluPProAsp 53
Db 242 AGCATTTGGAAGAGCGCCGAGCGCGGATTCATTGACCGGCGACCAAGCGGAAAAAGCAG 301
Qy 54 LeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTrrpGluProAspAspPhe 73
Db 302 ACTGCCACTTGTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 361
Qy 74 IleGluGluHisLysLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPhe 93
Db 362 TGGAAAGAGCAGCGGAAACATGACCCCAAGCGAGTTCCCAAGCTATGTCCTCCGAA 421
Qy 94 GluGluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
Db 422 AGGAATTAAACCGATACCAATTTCCTGGAATTCCTTGGAACCGTCTTAAGGACAGATA 481
Qy 114 AlaLysGluThrAsnAsnLysLysLysGluPhe---GluGluThrAlaLysLysVal 131
Db 482 GAAAAAGCTGCAAAAGCTTCAATCGAGCTTCCTTCGAGAGATGAGAGCGCTTA 538

RESULT 15
US-09-283-144-1
; Sequence 1, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for selectively Modulating the Interactions
; TITLE OF INVENTION: between Survivin and Tubulin
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880

; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: DNA sequence of proximal 5' flanking region of
; OTHER INFORMATION: Survivin gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (291)..(401)
US-09-283-144-1

Alignment Scores:
Pred. No.: 6,16e-20 Length: 417
Score: 221.00 Matches: 38
Percent Similarity: 92.86% Conservative: 1
Best Local Similarity: 90.48% Mismatches: 3
Query Match: 28.41% Indels: 0
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-283-144-1 (1-417)

QY 1 MetGlyAlaProThrLeuProAlaATPGlnProPheLeuLysAspHisArgIleSer 20
Db 291 ATGGTGCCCCCGCGCTGCCCCCTGCGACGCCCTTCTCAGAGACCCCGCATCTCT 350
QY 21 ThrPheLysAsnTrpProPheLeuGlnGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 351 ACATTCAAGACTGCGCCCTTCTTGAGGCGCTGCGCTGCACCCCGAGCGGAGTGAAGACTG 410
QY 41 AlaGly 42
Db 411 CCCGGC 416

Search completed: November 1, 2004, 19:18:42
Job time: 100 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 1, 2004, 20:31:52 ; Search time 369 Seconds
(without alignments)
1973.223 Million cells updates/sec

Title: US-09-690-825-34

Perfect score: 142
Sequence: 1 MGAFTLPAMQPLKDHRS.....EPETAKYRAIEDLAAMD 142

Scoring table:
Oligo Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 256380028 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6817622

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame_plus_p2n.model -DRV=xlp
-Q=/cgn2_1/USPTO.spool_p/US09690825/turnat_01122004_105500_2117/app_query.fasta_1.327
-DB=PubMed Applications NA -QFMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=equality -THR MIN=1
-ALIGN=15 -MODE=IOCL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09690825@cgn2_1.1.723@turnat_01122004_105500_2117
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Published Applications NA:
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq.*
13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
18: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	429	17 US-10-665-975-1	Sequence 1, Appl
2	142	100.0	1619	9 US-09-918-186A-97	Sequence 97, Appl
3	142	100.0	1619	15 US-10-181-316-97	Sequence 97, Appl
4	142	100.0	1619	15 US-10-172-118-566	Sequence 566, Appl
5	142	100.0	1619	15 US-10-388-360-324	Sequence 324, Appl
6	142	100.0	1619	16 US-10-342-887-566	Sequence 566, Appl
7	142	100.0	1619	16 US-10-283-975A-445	Sequence 445, Appl
8	142	100.0	1619	17 US-10-657-022-99	Sequence 99, Appl
9	142	100.0	1643	18 US-10-807-897-1	Sequence 1, Appl
10	142	100.0	2404	13 US-10-071-766-109	Sequence 109, Appl
11	142	100.0	2404	15 US-10-084-817-285	Sequence 285, Appl
12	128	90.1	2570	17 US-10-741-601-210	Sequence 210, Appl
13	128	90.1	2585	17 US-10-741-601-216	Sequence 216, Appl
14	113	79.6	578	17 US-10-741-601-213	Sequence 213, Appl
15	93	65.5	740	16 US-10-305-720-918	Sequence 918, Appl
16	74	52.1	2639	17 US-10-741-601-215	Sequence 215, Appl
17	74	52.1	2654	17 US-10-741-601-211	Sequence 211, Appl
18	73	51.4	2452	17 US-10-741-601-212	Sequence 212, Appl
19	73	51.4	2467	17 US-10-741-601-214	Sequence 214, Appl
20	41	28.9	955	9 US-09-918-186A-10	Sequence 10, Appl
21	41	28.9	955	15 US-10-181-316-10	Sequence 10, Appl
22	41	28.9	955	15 US-10-807-897-3	Sequence 3, Appl
23	40	28.2	121	15 US-10-179-730-33	Sequence 33, Appl
24	39	27.5	14795	15 US-10-181-316-3	Sequence 3, Appl
25	39	27.5	14796	9 US-09-954-456-973	Sequence 973, Appl
26	39	27.5	14796	9 US-09-954-456-1636	Sequence 1636, Appl
27	39	27.5	14796	9 US-09-918-186A-3	Sequence 3, Appl
28	39	27.5	14796	9 US-09-880-107-3421	Sequence 3421, Appl
29	39	27.5	14796	11 US-09-968-007A-522	Sequence 522, Appl
30	39	27.5	14796	15 US-10-138-618-35	Sequence 35, Appl
31	39	27.5	23393	17 US-10-741-601-5680	Sequence 5680, Appl
32	39	27.5	41399	15 US-10-741-601-5768	Sequence 5768, Appl
33	36	25.4	120	15 US-10-029-386-23672	Sequence 23672, A
34	36	25.4	555	15 US-10-029-386-9972	Sequence 9972, A
35	36	25.4	1100	14 US-10-108-877-2	Sequence 2, Appl
36	33	23.2	201	17 US-10-741-601-4404	Sequence 4404, A
37	33	23.2	201	17 US-10-741-601-4415	Sequence 4415, A
38	33	23.2	201	17 US-10-741-601-4451	Sequence 4451, A
39	33	23.2	201	17 US-10-741-601-4462	Sequence 4462, A
40	29	20.4	13575	17 US-10-741-601-4563	Sequence 4563, A
41	23	16.2	144	17 US-10-741-601-4411	Sequence 4411, A
42	23	16.2	144	17 US-10-741-601-4423	Sequence 4423, A
43	23	16.2	144	17 US-10-741-601-4434	Sequence 4434, A
44	23	16.2	144	17 US-10-741-601-4436	Sequence 4436, A
45	23	16.2	144	17 US-10-741-601-4447	Sequence 4447, A

ALIGNMENTS

RESULT 1
US-10-665-975-1
; Sequence 1, Application US/10665975
; Publication No. US2004013819A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Tamm, Ingo
; TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING
; TITLE OF INVENTION: PROTEIN (HEXIP) IN MODULATION OF APOPTOSIS
; FILE REFERENCE: BURHAM,005A
; CURRENT APPLICATION NUMBER: US/10/665,975
; PRIOR APPLICATION NUMBER: 2003-09-18
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-665-975-1

Alignment Scores:

Pred. No.: 5,61e-145 Length: 429
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-665-975-1 (1-429)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 1 ATGGGTGCCCCGAGAGTGGCCCCCTGGCTGGACGCCCTTTCTCAAGAGCACCGCATCTCT 60
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 61 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCCCTGGACCCCGAGCGGATGGCCGAG 120
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 121 GCTGGCTTCATCCACTGCCCTCACTGAGACGAGCCGACCTTGCCCGAGTCTTCTTCTGC 160
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80
DB 181 TTCAAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGAACTAATAAAGCAT 240
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 241 TCGTCGGGTTCGGCTTTCCTTCTTGTCAAGAGAGAGTTGAAGATTAACTTGGTGA 300
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 301 TTTTGAACCTGGACAGAAAGAAAGCCAGCAAAATTGCAGAGAAACCAACATTAAG 360
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140
DB 361 AAGAAAGAAATTGAGAAAGCTGGAGAAAGTGGCCGCTGCATCGAGCGTGGCTGCC 420
QY 141 MetAsp 142
DB 421 ATGGAT 426

RESULT 2

US-09-918-186A-97
; Sequence 97, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 97
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-186A-97

Alignment Scores:
Pred. No.: 1.89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Mismatches: 0
Indels: 0
Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-186A-97 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCGAGAGTGGCCCCCTGGCTGGACGCCCTTTCTCAAGAGCACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCCCTGGACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GCTGGCTTCATCCACTGCCCTCACTGAGACGAGCCGACCTTGCCCGAGTCTTCTTCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80
DB 230 TTCAAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGAACTAATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGTCGGGTTCGGCTTTCCTTCTTGTCAAGAGAGAGTTGAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 350 TTTTGAACCTGGACAGAAAGAAAGCCAGCAAAATTGCAGAGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140
DB 410 AAGAAAGAAATTGAGAAAGCTGGAGAAAGTGGCCGCTGCATCGAGCGTGGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 3

US-10-181-316-97
; Sequence 97, Application US/10181316
; Publication No. US20030211607A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0650
; CURRENT APPLICATION NUMBER: US/10/181,316
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02939
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 97
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-181-316-97

Alignment Scores:
Pred. No.: 1.89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-97 (1-1619)

```
QY 1 MetGlyAlaProThrLeuProProAlaATrpgInProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGACGTTGCCCCCTGCTGCGACGCTTTCTCAAGACCAACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGGTGGCCCTGACACCCCGAAGCGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACGCCCCCACTGGAAGACGACCCGACTGGCCCGAGTTCCTTCCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGAGCTGGAAAGCTGGAGCCAGCATGACGACCCCAATGAGGAACATTAATAAACAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGCTTCTTCTGTCAGAACAGATTGAAGATTAAACCTTGATGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 350 TTTTGAACCTGACACAGAAAGCCCAAGAACAAATTGCAAGGAAACCAACATAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGAAACTGCAAGAAAGTCCGCGTCATCGACGACGCTGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475
```

RESULT 4

```
US-10-172-118-566
/ Sequence 566, Application US/10172118
/ Publication No. US20030224374A1
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: He, Yudong
/ APPLICANT: Linsley, Peter
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Chris
/ APPLICANT: Van 't Veer, Laura
/ APPLICANT: Van de Vijver, Marc
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-175-999
/ CURRENT APPLICATION NUMBER: US/10/172,118
/ PRIOR FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/380,770
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 566
/ LENGTH: 1619
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ENTRY DATE: 2001-06-18
/ US-10-172-118-566
```

Alignment Scores:

```
Pred. No.: 1,89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
```

US-09-690-825-34 (1-142) x US-10-172-118-566 (1-1619)

```
QY 1 MetGlyAlaProThrLeuProProAlaATrpgInProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGACGTTGCCCCCTGCTGCGACGCTTTCTCAAGACCAACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGGTGGCCCTGACACCCCGAAGCGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACGCCCCCACTGGAAGACGACCCGACTGGCCCGAGTTCCTTCCTGC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGAGCTGGAAAGCTGGAGCCAGCATGACGACCCCAATGAGGAACATTAATAAACAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGCTTCTTCTGTCAGAACAGATTGAAGATTAAACCTTGATGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 350 TTTTGAACCTGACACAGAAAGCCCAAGAACAAATTGCAAGGAAACCAACATAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGAAACTGCAAGAAAGTCCGCGTCATCGACGACGCTGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475
```

RESULT 5

```
US-10-388-360-324
/ Sequence 324, Application US/10388360
/ Publication No. US20030225528A1
/ GENERAL INFORMATION:
/ APPLICANT: GENOMIC HEALTH
/ APPLICANT: Baker, Joffrey B.
/ APPLICANT: Cronin, Maureen T.
/ APPLICANT: Kiefer, Michael C.
/ APPLICANT: Shak, Steve
/ APPLICANT: Walker, Michael Graham
/ TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
/ FILE REFERENCE: 39740-0001US
/ CURRENT APPLICATION NUMBER: US/10/388,360
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 60/412,049
/ PRIOR FILING DATE: 2002-09-18
/ PRIOR APPLICATION NUMBER: US 60/364,890
/ PRIOR FILING DATE: 2002-03-13
/ NUMBER OF SEQ ID NOS: 384
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 324
/ LENGTH: 1619
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-388-360-324
```

Alignment Scores:

```
Pred. No.: 1,89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
```

US-09-690-825-34 (1-142) x US-10-388-360-324 (1-1619)

```
QY 1 MetGlyAlaProThrLeuProProAlaATrpgInProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGACGTTGCCCCCTGCTGCGACGCTTTCTCAAGACCAACCGCATCTCT 109
```

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GCTGGCTTCATCCACTGCTCCCACTGAGAACGACGACACTGGCCCGAGTGTCTTCTGCG 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80
DB 230 TTCAGAGAGCTGGAAGCTGGAGCCGACGATGACGCCCATGAGAACTTAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGCCCGCTTCCGCTTCTTCTGTCAGAGAACAGTTGAAAGATTACCTTGTTGAA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 350 TTTTGAACCTGGACAGAGAAAGAGCCAGAACAAATTCGAAAGGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140
DB 410 AAGAAAGATTGAGAGAACTGCGAAGAAAGTCCGCGCTGCATCGAGAGCTGGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 5

US-10-342-887-566
; Sequence 566, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yidong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 566
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-566

Alignment Scores:

Pred. No.: 1,89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-342-887-566 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCGCCGACGTTGCGCCCTGCGAGCGCTTCTTCAAGAGCAACCGCATCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GCTGGCTTCATCCACTGCTCCCACTGAGAACGACGACACTGGCCCGAGTGTCTTCTGCG 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80
DB 230 TTCAGAGAGCTGGAAGCTGGAGCCGACGATGACGCCCATGAGAACTTAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 290 TCGCCCGCTTCCGCTTCTTCTGTCAGAGAACAGTTGAAAGATTACCTTGTTGAA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 350 TTTTGAACCTGGACAGAGAAAGAGCCAGAACAAATTCGAAAGGAAACCAACATTAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140
DB 410 AAGAAAGATTGAGAGAACTGCGAAGAAAGTCCGCGCTGCATCGAGAGCTGGCTGCC 469
QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 7

US-10-283-975A-445
; Sequence 445, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 445
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-445

Alignment Scores:

Pred. No.: 1,89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-283-975A-445 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCGCCGACGTTGCGCCCTGCGAGCGCTTCTTCAAGAGCAACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 170 GCTGGCTTCATCCACGCGCCCACTGGAACGAGCAGACTTGCGCCAGGTTCTTCGCG 229

Qy 61 PheLysGluLeuGlnGlyTTPGluProAspAspProIleGluGlnHisLysLysHis 80

Db 230 TTTCAAGAGCTGGAGAGCTGGAGAGCTGACGACCCCATAGAGACATTAAGCAT 289

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 290 TCGTCGGGTGGCTTCTTCCTTCTGTCAGAGACAGATTGAAGAAATTAACCTTGTA 349

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

Db 350 TTTTGAAGACTGGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATTAAG 409

Qy 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140

Db 410 AAGAAGAAATTTGAGAAACTGGAAGAAAGTGGCGCCGTCATGAGCAGCTGGCTGCC 469

Qy 141 MetAsp 142

Db 470 ATGGAT 475

RESULT 8

US-10-657-022-99

/ Sequence 99, Application US/10657022

/ Publication No. US20040180354A1

/ GENERAL INFORMATION:

/ APPLICANT: Simard, John J. L.

/ APPLICANT: Diamond, David C.

/ APPLICANT: Liu, Liping

/ TITLE OF INVENTION: EPTROPE SEQUENCES

/ FILE REFERENCE: MANKK.032A

/ CURRENT APPLICATION NUMBER: US/10/657,022

/ CURRENT FILING DATE: 2003-09-04

/ PRIOR APPLICATION NUMBER: 60/409123

/ PRIOR FILING DATE: 2002-09-06

/ NUMBER OF SEQ ID NOS: 610

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 99

/ LENGTH: 1619

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-657-022-99

Alignment Scores:

Pred. No.: 1,89e-144 Length: 1619

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Db: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-657-022-99 (1-1619)

Qy 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20

Db 50 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGCCCTTTCTCAAGACCAACCCGATCT 109

Qy 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCTGCAACCCGAGAGCGATGGCGAG 169

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 170 GCTGGCTTCATCCACGCGCCCACTGGAACGAGCAGCTTGCCCAAGTCTTCTTCG 229

Qy 61 PheLysGluLeuGlnGlyTTPGluProAspAspProIleGluGlnHisLysLysHis 80

Db 230 TTTCAAGAGCTGGAGAGCTGGAGACGATGACGACCCCATAGAGAACTTAAGCAT 289

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 290 TCGTCGGGTGGCTTCTTCCTTCTGTCAGAGACAGATTGAAGAAATTAACCTTGTA 349

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

Db 350 TTTTGAAGACTGGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATTAAG 409

Qy 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140

Db 410 AAGAAGAAATTTGAGAAACTGGAAGAAAGTGGCGCCGTCATGAGCAGCTGGCTGCC 469

Qy 141 MetAsp 142

Db 470 ATGGAT 475

RESULT 9

US-10-807-897-1

/ Sequence 1, Application US/10807897

/ Publication No. US20040192631A1

/ GENERAL INFORMATION:

/ APPLICANT: Xiang, Rong

/ APPLICANT: Zhou, He

/ APPLICANT: Reisfeld, Ralph A.

/ TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND

/ TITLE OF INVENTION: METHODS OF USE THEREOF

/ FILE REFERENCE: TSRI-874.1

/ CURRENT APPLICATION NUMBER: US/10/807,897

/ CURRENT FILING DATE: 2004-03-24

/ PRIOR APPLICATION NUMBER: 60/457,009

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 29

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 1

/ LENGTH: 1643

/ TYPE: DNA

/ ORGANISM: HOMO SAPIENS

US-10-807-897-1

Alignment Scores:

Pred. No.: 1,92e-144 Length: 1643

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Db: 18 Gaps: 0

US-09-690-825-34 (1-142) x US-10-807-897-1 (1-1643)

Qy 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20

Db 45 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGCCCTTTCTCAAGACCAACCCGATCT 104

Qy 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 105 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCTGCAACCCGAGAGCGATGGCGAG 164

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 165 GCTGGCTTCATCCACGCGCCCACTGGAACGAGCAGCTTGCCCAAGTCTTCTTCG 224

Qy 61 PheLysGluLeuGlnGlyTTPGluProAspAspProIleGluGlnHisLysLysHis 80

Db 225 TTTCAAGAGCTGGAGAGCTGGAGACGATGACACCCCATAGAGAACTTAAGCAT 284

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 285 TCGTCGGGTGGCTTCTTCCTTCTGTCAGAGACAGATTGAAGAAATTAACCTTGTA 344

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

Db 345 TTTTGAAGACTGGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATTAAG 404

Qy	121	LySLySGIaPhneIuGluThzAlaYsLySVaIaAGAGAlaIeGIuGLEuAlaA	140
Qy	405	AAAGAAATTTAGGAAACTGGAAAGAGCGCCCGCATGACCACTGGCTGCC	466
Db			
Qy	141	MetAsp	142
Db	465	ATGAGT	470

RESULT 10

```

US-10-071-766-109
Sequence 109, Application US/10071766
Publication No. US20020192678A1
GENERAL INFORMATION:
APPLICANT: Huel-Wei Chen
FILE OF INVENTION: GENES EXPRESSED IN SENESENCE
TITLE REFERENCE: PA-0043 US
CURRENT APPLICATION NUMBER: US/10/071,766
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ. ID NOS: 144
SOFTWARE: PERL Program
SEQ. ID NO: 109
LENGTH: 2404
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Indyle ID No. US20020192678A1 251651.4
NAME/KEY: unsure
LOCATION: 710, 717, 724, 982-1007
OTHER INFORMATION: a, t, c, g, or other
US-10-071-766-109

```

Alignment Scores:	
Pred. No.:	2,71e-14
Score:	142.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	13
Length:	240
Matches:	142
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-690-825-34 (1-142) X US-10-071-766-109 (1-2404)

QY	MeG A A Prothr Leu Pro Pro Ala Tyr Gln Pro Phe Leu Lys Asp His Arg Leu Ser	20
Db	ATGGGTGCCCCGACCTGGCCCCCTGGCTGGACGCCCTTTCGACGACACCGCATCTCT	115
QY	21 Thr Phe Lys Asn Tyr Pro Phe Leu Gln Gly Cys Ala Cys Thr Pro Gln Arg Met Ala Glu	40
Db	ACATTCACAGACCTGGCCCTCTTCTTGGAGGGCTGCTGCTCACCCCGAGCGGATGGCGAG	175
QY	41 Ala G A Phe Leu His Cys Pro Thr Gln Gln Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys	60
Db	GCTGGCTTCATCCACTGGCCCACTGACGACGACGACCTGGCCCACTGTTTCTTCTGC	235
QY	61 Phe Lys Glu Leu Gln Glu Tyr Tyr Glu Pro Asp Asp Asp Pro Leu Gln His Lys Lys His	80
Db	TTCACGAGCTGGAAAGCTGGGAGCCAGATGACGACCCCATATGAGAACATATMAAACAT	295
QY	81 Ser Ser Gly Cys Ala Phe Leu Ser Val Lys Lys Gln Phe Gln Glu Leu Thr Leu Gly Glu	100
Db	TCGTCCGGTGGCCCTTCTCTTCTGTGCAGGAAGCGTTGAGAGATTAAACCTTGGTGAA	355
QY	101 Phe Leu Lys Leu Asp Arg Glu Arg Ala Lys Asn Lys Ile Ala Lys Glu Thr Asn Asn Lys	120
Db	TTTTTGAACCTGCACGAGAAAGAGCCAGAACAAATTTGCAGAGAAACCAACATATGAG	415
QY	121 Lys Lys Glu Phe Gln Glu Thr Ala Lys Lys Val Arg Arg Ala Ile Glu Gln Leu Ala Ala	140
Db	AACAAAGAAATTTGAGGAAACCTCGAAGAAAGTCCCTCGCCATCGAGCACTGGCTGCC	475
QY	141 Met Asp	142
Db	ATGGAT	481

RESULT 11
US-10-084

```

US-10-084-817-285
Sequence 285, Application US/10084817
Publication No. US20030119009A1
GENERAL INFORMATION:
APPLICANT: Susan Stuart
APPLICANT: Jed G. Nucleon
APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 285
LENGTH: 2404
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Indyle ID NO. US20030119009A1 251651.4
NAME/KEY: unsure
LOCATION: 710, 717, 724
OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-285

```

Alignment Scores:	
Pred. No.:	2,71e-14
Score:	142.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
GB:	15
Length:	2404
Matches:	142
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-690-825-34 (1-142) X US-10-084-817-285 (1-2404)

QY	21	MetGLVAlaProThrLeuProPheProAlaIrrpGlnProPheLeuLysAspHisArgIleSer	20
Db	56	ATGGAGGCCCCAGACGTTGCCCCCTCCCTGGACAGCCCTTTCTCAAGACACACCGCATCTCT	115
QY	21	ThrPheLysAsnTrrProPheLeuGluGlyCysAlaCysThrProGluIuaIrgMetAlaGlu	40
Db	116	ACATTTCAAAACCTGGCGCTTCTTTGGAGGGCTGGCGCTTGACACCCGGAGCGGATGGCCGAG	175
QY	41	AlaGlyPheIleHisCysProThrGluIuaGngIuProAspIleuAlaGlnCysPhePheCys	60
Db	176	GCTGGCTTATTCACCTGCCCCCACTAGAACAGACCACTGGCCCCAGTGTGTTCTTCTGCG	235
QY	61	PheLysGluLeuGluGluYrrpGluIuProAspAspProIleGluGluHisLysLysHis	80
Db	236	TTTCAAGACACTGGAAAGGCTGGAGGACCAAGATACGACCCCATAGAGGAACATATAAAACCAT	295
QY	81	SetSerGlyCysAlaPheLeuSerAlaLysLysGlnPheGluGluIuaIrrLeuGlyGlu	100
Db	296	TGCTCCGGATTGGCGCTTCTCTCTCTCAAGAACGATTGGAAAGATTAAACCTTGCGTGA	355
QY	101	PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys	120
Db	356	TTTTTAACCTGACAGAGAAAGAACCCCAAGAACAAATATTCGAAGAGAAACCAACAAATAG	415
QY	121	LysLysGluIuPheGluGluThrAlaLysLysValArgArgAlaIleGluGluIuLeuAlaAla	140
Db	416	AACAAAGAAATTGAGGAAACTGGCAAGAAAGTGGCGCTGGCATCGAGACACTGGCTGCC	475
QY	141	MetAsp	142
Db	476	ATGGAT	481
RESULT	12		


```
US-10-741-601-210
; Sequence 210, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 4,83e-129 Length: 2570
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.14% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-210 (1-2570)
QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGAGCTGGCCCTTCCCTGCGAGCCCTTCTCAAGAGCACCAGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCCCTGACACCCCGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheUlaGlnCysPhePheCys 60
DB 195 GCTGCTTCATCCACTGCCCCCACTGAGAACGAGCCAGACTGGCCCAAGTTCTCTCTGC 254
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluIuHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATTAAGAGAACTAAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCCTCCGCTGGCGCTTCTCTTCTGTCAGAGAACAGATTGAAGATTAACTTGGTGA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 375 TTTTGAAGAACTGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATAAG 434
QY 121 LysLysGluPheGluGluThrAla 128
DB 435 AAGAAAGAAATTGAGGAAACTGCG 458
;
RESULT 13
US-10-741-601-216
; Sequence 216, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 2585
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 4,86e-129 Length: 2585
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.14% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-216 (1-2585)
QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGAGCTGGCCCTTCCCTGCGAGCCCTTCTCAAGAGCACCAGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCCCTGACACCCCGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheUlaGlnCysPhePheCys 60
DB 195 GCTGCTTCATCCACTGCCCCCACTGAGAACGAGCAAGCTTGGCCCATGTTCTTCTTGC 254
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluIuHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATTAAGAGAACTAAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCCTCCGCTGGCGCTTCTCTTCTGTCAGAGAACAGATTGAAGATTAACTTGGTGA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 375 TTTTGAAGAACTGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATAAG 434
QY 121 LysLysGluPheGluGluThrAla 128
DB 435 AAGAAAGAAATTGAGGAAACTGCG 458
;
RESULT 14
US-10-741-601-213
; Sequence 213, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 2,53e-113 Length: 578
Score: 113.00 Matches: 113
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.58% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-213 (1-578)
QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGAGCTGGCCCTTCCCTGCGAGCCCTTCTCAAGAGCACCAGCATCTCT 134
```

```
US-10-741-601-216
; Sequence 210, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 4,83e-129 Length: 2570
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.14% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-210 (1-2570)
QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGAGCTGGCCCTTCCCTGCGAGCCCTTCTCAAGAGCACCAGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCCCTGACACCCCGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheUlaGlnCysPhePheCys 60
DB 195 GCTGCTTCATCCACTGCCCCCACTGAGAACGAGCCAGACTGGCCCAAGTTCTCTCTGC 254
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluIuHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATTAAGAGAACTAAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCCTCCGCTGGCGCTTCTCTTCTGTCAGAGAACAGATTGAAGATTAACTTGGTGA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 375 TTTTGAAGAACTGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATAAG 434
QY 121 LysLysGluPheGluGluThrAla 128
DB 435 AAGAAAGAAATTGAGGAAACTGCG 458
;
RESULT 14
US-10-741-601-213
; Sequence 213, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 2,53e-113 Length: 578
Score: 113.00 Matches: 113
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.58% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-213 (1-578)
QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGAGCTGGCCCTTCCCTGCGAGCCCTTCTCAAGAGCACCAGCATCTCT 134
```

QY 21 ThrPheLysAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 Db 135 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCCCGACCCCGAGCGAGTGGCCGAG 194
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 Db 195 GCTGGCTTCATCCCTCCCGACACGAGAGACGAGCAGACTTGGCCCGAGTCTTCTCTG 254
 QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80
 Db 255 TTCAAGAGAGCTGGAGGCTGGAGCCGACATGACGCCCATAGAGAACTATAAAGCAT 314
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100
 Db 315 TCGTCCGCTGGCTTCCCTTCTTCTGTCAGAGAGAGCTTTCAGAGATTAACTTGGTGA 374
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
 Db 375 TTTTGAACCTGACAGAGAAAGAGCCAGAACAAAT 413

RESULT 15

US-10-305-720-918
 / Sequence 918, Application US/10305720
 / Publication No. US20040010136A1
 / GENERAL INFORMATION:
 / APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 / TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
 / FILE REFERENCE: PA-0002-1 CON
 / CURRENT APPLICATION NUMBER: US/10/305,720
 / PRIOR FILING DATE: 2002-11-26
 / PRIORITY APPLICATION NUMBER: 09/016,434
 / NUMBER OF SEQ ID NOS: 1490
 / SOFTWARE: PERL Program
 / SEQ ID NO 918
 / LENGTH: 740
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / OTHER INFORMATION: Incyte ID No. US20040010136A1 752848
 / NAME/KEY: unsure
 / LOCATION: (1) ... (740)
 / OTHER INFORMATION: a, t, c, g, or other
 US-10-305-720-918

Alignment Scores:

Pred. No.: 1,78e-91 length: 740
 Score: 93.00 Matches: 130
 Percent Similarity: 98.48% Conservative: 0
 Best Local Similarity: 98.48% Mismatches: 1
 Query Match: 65.49% Indels: 2
 DB: 16 Gaps: 0

US-09-690-825-34 (1-142) * US-10-305-720-918 (1-740)

QY 12 ProPheLeuLysAspHisArgIleSerThrPheLysAsnTPProPheLeuGluGlyCys 31
 Db 51 CCGCTTCTCAAGAGCACCGCATCTCTACATCAAGAACTGGCCCTTCTGGAGGGCTGC 110
 QY 32 AlaGlyThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGlu-AsnG 51
 Db 111 GCGTGCACCCCGAGCGGATGCGCGAGGCTGGCTTCATCCACTGCCCCACTGA-NAACGA 169
 QY 51 uProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTTPGluProAsp 71
 Db 170 GCCAGACTTGGCCCGAGTCTTCTCTCTCTCAAGAGAGCTGGAAGGCTGGAGCCAGATGA 229
 QY 71 pAspProIleGluGluHisLysLysSerSerGlyCysAlaPheLeuSerValLysLys 91
 Db 230 CGACCCCATAGAGGAACATAAAGCAATTCGCTGGCTTCTTCTGTCAGAA 289

QY 91 sGlnPheGluGluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAs 111
 Db 290 GCAGTTTGAAAGATTAACTCTTGTGATTTTGAACCTGACACGAGAAAGGCCAAAGAA 349
 QY 111 nLysIleAlaLysGluThrAsnAsnLysLysLysGluPheGluGluThrAlaLysLysVa 131
 Db 350 CAAATTTCCAAAGAGAAACCAATTAAGAAAGAAATTTGAGGAAACTGGAGAAAGAGT 409
 QY 131 lArgArgAlaIleGluGluLeuAlaAlaMetAsp 142
 Db 410 GCGCGTGCATCGAGCGAGCTGGCTGCCATGAT 443

Search completed: November 1, 2004, 21:47:03
 UOD time : 373 secs

Tue Nov 2 12:23:18 2004

us-09-690-825-34.rn1

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: November 1, 2004, 19:17:01 ; Search time 89 Seconds
(without alignments)
1134.068 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142
Sequence: 1 MAGFLPMAOPFLXDRHS.....EFETAKVRAIEQLAAMD 142

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delcp 6.0 , Delext 7.0

Searched: 824507 segs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1643611

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=fixme+ p2n.model -DEV=xlp
-CGN2_1/USPTO.spool/p/US09690825/unat 0112004 105458 2076/app.query.fasta_1.327
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=cdi -MINMATCH=0.1 -LOOPTCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09690825.CCN_1_1_105.@runat 0112004 105458 2076 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBILOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA.*
1: /cgn2_6/prodata/1/ina/58_COMB.seq.*
2: /cgn2_6/prodata/1/ina/58_COMB.seq.*
3: /cgn2_6/prodata/1/ina/68_COMB.seq.*
4: /cgn2_6/prodata/1/ina/68_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCOTUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfills1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	142	100.0	426	US-09-283-144-2	Sequence 2, Appl1
2	142	100.0	426	US-09-163-162-1	Sequence 1, Appl1
3	142	100.0	426	US-09-286-407-1	Sequence 1, Appl1
4	142	100.0	426	US-09-496-694B-97	Sequence 97, Appl1
5	107	75.4	1165	US-08-448-722A-1	Sequence 1, Appl1
6	107	75.4	1165	US-08-189-305B-1	Sequence 1, Appl1
7	93	65.5	740	US-09-016-434-918	Sequence 918, Appl1
8	76	53.5	399	US-09-513-999C-2315	Sequence 2315, Appl1
9	41	28.9	955	US-09-496-694B-10	Sequence 10, Appl1
10	39	27.5	14796	US-08-975-080-35	Sequence 35, Appl1
11	39	27.5	14796	US-09-630-706-10	Sequence 10, Appl1
12	39	27.5	14796	US-09-496-694B-3	Sequence 3, Appl1

13	37	26.1	417	US-09-283-144-1	Sequence 1, Appl1
14	9	6.3	30	US-09-672-717-199	Sequence 199, Appl1
15	8	5.6	26	US-09-496-694B-13	Sequence 13, Appl1
16	8	5.6	293	US-09-621-976-13359	Sequence 13359, A
17	8	5.6	326	US-09-621-976-13398	Sequence 13398, A
18	8	5.6	337	US-09-621-976-13384	Sequence 13384, A
19	8	5.6	342	US-09-621-976-13367	Sequence 13367, A
20	8	5.6	346	US-09-621-976-13443	Sequence 13443, A
21	8	5.6	349	US-09-621-976-13375	Sequence 13375, A
22	8	5.6	351	US-09-621-976-13420	Sequence 13420, A
23	8	5.6	357	US-09-621-976-13407	Sequence 13407, A
24	8	5.6	361	US-09-621-976-13392	Sequence 13392, A
25	8	5.6	365	US-09-621-976-13428	Sequence 13428, A
26	8	5.6	515	US-09-496-694B-231	Sequence 231, Appl
27	8	5.6	707	US-09-270-767-11365	Sequence 11365, A
28	8	5.6	812	US-09-270-767-15067	Sequence 15067, A
29	8	5.6	4376	US-08-119-125A-2	Sequence 1, Appl1
30	8	5.6	6744	US-08-119-125A-2	Sequence 2, Appl1
31	7	4.9	21	US-09-163-162-2	Sequence 2, Appl1
32	7	4.9	21	US-09-286-407-2	Sequence 2, Appl1
33	7	4.9	21	US-09-496-694B-4	Sequence 4, Appl1
34	7	4.9	22	US-09-163-162-3	Sequence 3, Appl1
35	7	4.9	22	US-09-286-407-3	Sequence 3, Appl1
36	7	4.9	22	US-09-496-694B-5	Sequence 5, Appl1
37	7	4.9	23	US-09-163-162-4	Sequence 4, Appl1
38	7	4.9	23	US-09-286-407-4	Sequence 4, Appl1
39	7	4.9	23	US-09-496-694B-6	Sequence 6, Appl1
40	7	4.9	29	US-10-270-313-2	Sequence 2, Appl1
41	7	4.9	222	US-09-513-999C-29674	Sequence 29674, A
42	7	4.9	273	US-09-313-294A-1818	Sequence 1818, Appl
43	7	4.9	310	US-09-328-111-715	Sequence 715, Appl
44	7	4.9	504	US-09-107-532A-1578	Sequence 1578, Appl
45	7	4.9	559	US-09-621-976-10449	Sequence 10449, A

ALIGNMENTS

Result 1
US-09-283-144-2
; Sequence 2, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; FILE REFERENCE: 44574-5033-US
; CURRENT FILING DATE: 1999-04-01
; EARLIER FILING DATE: 1999-04-01
; EARLIER FILING DATE: 1998-04-01
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of open reading frame encoding
; OTHER INFORMATION: Survivin
US-09-283-144-2
Alignment Scores:
Pred. No.: 3,91e-141 Length: 426
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-283-144-2 (1-426)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 1 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGCCCTTTCTCAAGAGCCACCCGATGCTCT 60

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 61 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCGCTGCACCCCGGAGCGGATGGCCGAG 120

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 121 GCTGCGTTCACTCCCTCCCACTGAGAACGAGCCAACTGGCCCACTTTCTTCTGCTG 180

QY 61 PheLeuLysLeuGluGlyTrpGluProAspAspProIleGluGluHis 80
DB 181 TTCAAGAGCTGGAGGCTGGAGCCAGATGACACCCCATAGAGAACTAAAGAAAGCAT 240

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGluGlu 100
DB 241 TCGTCCGTTGCGCTTCTTCTTCTGTCAGAGAGCTTTAAGATTAACTTGGTGA 300

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 301 TTTTGAAGACTGACAGAGAAAGAGCCAGCAAAATTGCAAGGAAACCAATTAAG 360

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
DB 361 AAGAAAGATTTTGAGAACTGCGAAGAAAGTGGCGCTGCATCGAGCAGCTGGCTGCC 420

QY 141 MetAsp 142
DB 421 ATGGAT 426

RESULT 2

US-09-163-162-1

Sequence 1, Application US/09163162

Patent No. 6077709

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Swayze, Eric E.

APPLICANT: Cowser, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION

FILE REFERENCE: RTS-0008

CURRENT APPLICATION NUMBER: US/09/163,162

CURRENT FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 1

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (50)..(478)

US-09-163-162-1

Alignment Scores:

Pred. No.: 1,35e-140 Length: 1619

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-163-162-1 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGCCCTTTCTCAAGAGCCACCCGATGCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCGCTGCACCCCGGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GCTGCGTTCACTCCCTCCCACTGAGAACGAGCCAGCTGGCCCGATGTTCTTCTGCTG 229

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80
DB 220 TTCAAGAGCTGGAGGCTGGAGCCAGATACACCCCATAGAGAACTAAAGAAAGCAT 289

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGluGlu 100
DB 220 TCGTCCGTTGCGCTTCTTCTTCTGTCAGAGAGCTTTAAGATTAACTTGGTGA 349

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 350 TTTTGAAGACTGACAGAGAAAGAGCCAGCAAAATTGCAAGGAAACCAATTAAG 409

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
DB 410 AAGAAAGATTTTGAGAACTGCGAAGAAAGTGGCGCTGCATCGAGCAGCTGGCTGCC 469

QY 141 MetAsp 142
DB 470 ATGGAT 475

RESULT 3

US-09-286-407-1

Sequence 1, Application US/09286407A

Patent No. 6165788

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Swayze, Eric E.

APPLICANT: Cowser, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF Survivin EXPRESSION

FILE REFERENCE: ISPH-0349

CURRENT APPLICATION NUMBER: US/09/286,407A

CURRENT FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 1

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (50)..(478)

US-09-286-407-1

Alignment Scores:

Pred. No.: 1,35e-140 Length: 1619

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-286-407-1 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 50 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGCCCTTTCTCAAGAGCCACCCGATGCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCGCTGCACCCCGGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 170 GCTGCGTTCACTCCCTCCCACTGAGAACGAGCCAGCTGGCCCGATGTTCTTCTGCTG 229

QY	61	PhelYsGIuIeuuIuGIYtYrpgIuPcAaPAPaPpPcIleGIuGIuHtYsYLeYsHs	80
Db	230	TTCAAGAGCTGGAAAGCTGGAGCCAGATGACGCCCATAGAGAACATATAAACAT	289
QY	81	Se-Se-GIYcYsAlaPheIeuSeVallyIsYsGIuPheGIuIeuYtHleuGIYGIu	100
Db	290	TCGCTCGGTTGCCCTTCTCTTCTGCAAGAGCGATTGAGAAATTAACTCTTGCGAA	349
QY	101	PheIeuIyIeuuSpaYrGIuYrGAtaIySaenYsIleAtaYsGIuYtHraSpaYs	120
Db	350	TTTTGAAACTGACACGAGAAAGGCCAAGAACAAATTGCAAGAGAAACCAATATAG	409
QY	121	LysIySGIuPheGIuIuYtHraIaIySyaIaYrGArGAtaIleGIuIeuIaIaIa	140
Db	410	AACAAAGAAATTGAGAAACTGCGAAAGAAAGTGCCTGCGCATGAGACACTGGCTGCC	469
QY	141	MeLasp	142
Db	470	ATGGAT	475

```

RESULT 4
US-09-496-694B-97
: Sequence 97, Application US/0949694B
: Parent No. 635194
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: APPLICANT: Elizabeth J. Ackermann
: APPLICANT: Eric E. Swazey
: APPLICANT: Lex M. Cowser
: TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
: FILE REFERENCE: ISPH-0439
: CURRENT APPLICATION NUMBER: US/09/496,694B
: PRIOR FILING DATE: 2000-02-02
: PRIOR APPLICATION NUMBER: 09/286,407
: PRIOR FILING DATE: 1999-04-05
: PRIOR APPLICATION NUMBER: 09/163,162
: PRIOR FILING DATE: 1998-09-29
: NUMBER OF SEQ ID NOS: 249
: SEQ ID NO 97
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-496-694B-97

```

Pred. No.:	1,35e-140	Length:	1619
Score:	142.00	Matches:	142
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
GB:	3	Gaps:	0

US-09-690-825-34 (1-142) X US-09-496-694B-97 (1-1619)

Qy	MeGtAlaAaProThrLeuProPcoAlaTPrGInProPheLeuLysAShS;Arg1Ser 20
Db	50 ATGGGGGCCCGACGCTGGCCCCCTGGCTGGACGCCCTTTCACAGACACCGCATCTC 109
Qy	21 ThrPheLysAntTPrProPheLeuGluGlyCyAlaCySthrProGluArgMetAlaGlu 40
Db	110 ACATTCAAGAACTAGCGCCCTTCTTGGAGGGCTCGGCTCACCCCGAGCGGATGGCGAG 169
Qy	41 AlaGlyPheIleHisCysPProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db	170 GCTGGCTTCACTCCACTGCCCCCTGAGAACGACGACGACCTGGCCCCAGTGTTCCTTC 229
Qy	61 PheLysGluLeuGluGluGlyTPrGluProAspAspProIleGluGluHisLysLysHis 80
Db	230 TTCAAGAGAGCTGGAAGGCTGGGAGCCAGATGACGCCCATGAGAGAACTATTAAGACAT 289
Qy	81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db	290 TCGTCGGGTGGCGTTCTCTTCTTGTCACAAAGACAGTTGAAGAAATTAACCTTGGTGA 349

Qy	101	PheLeuIyLeuAspArgGluuArgAlaIyAsnIyIeAlaIyGluuTrpAsnIyLe	120
Db	350	TTTTGAAACTGGACAGCAAGAGACCAAGACAAATTTGAAAGGAAACCAACAATAG	409
Qy	121	IyLeIyGluPheGluGluTrpAlaIyIyIyValIyArgArgAlaIleGluGluLeuAla	140
Db	410	MAAAAGAAATTTGAGAAACTGCCGAAGAAAGTGGCCCGTCATCGACAGCTGGCTGCC	468
Qy	141	MetAsp	142
Db	470	ATGCAAT	475

RESULT 5
 US-08-448-722A-1/c
 : Sequence 1, Application US/08448722A
 : Patent No. 6072028
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Altieri, Dario C.
 : TITLE OF INVENTION: No. 6072028e1 Cell Surface Receptor, Antibody
 : TITLE OF INVENTION: Compositions, and Methods of Using Same
 : NUMBER OF SEQUENCES: 5
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Office of Patent Counsel, The Scripps
 : ADDRESS: Research Institute
 : STREET: 10550 No. 6072028ch Torrey Pines Road, TPC-8
 : CITY: La Jolla

ZIP: 92037

```

;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;

```

APPLICATION NUMBER: US/08/448,722A
FILING DATE: 25-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/189,309
FILING DATE: 30-JAN-1994

ATTORNEY/AGENT INFORMATION:
FILING DATE: 28-JAN-1994

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: 22

TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS: 1165 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

```

; TOPOLOGY: linear

```

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

	NAME/KEY:	CDS
;		
LOCATIONS		
07		1044

LOCATION:
MS-08-448-722A-1

T-Y771-044-00-00

Alignment Scores:

Pred. No.:	8.7e-104
------------	----------

Score:	107.00
Percent Similarity:	99.28%

```
Percent Similarity: 99.20%
Best Local Similarity: 99.28%
```

Query Match: 75.358

DB: 3

US-09-690-825-34 (1-142) X US-08-448-722A-1 (1-1165)

Pred. No.:	8.7e+04	length:	11
Score:	107.00	Matches:	13
Percent Similarity:	99.68%	Conservative:	0
Best local Similarity:	99.28%	Mismatches:	1
Query Match:	75.35%	Indels:	0
DB:		Gaps:	0

```

QY      1 MetGlyAlaProThrIleuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB      1114 ATGGGTCCCGCCGAGCTTGGCCCTGCTGCGAGCCCTTTTCTCAAGAACACCCGATCTCT 1055
QY      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB      1054 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCC-TCGACCCCGAGCGATGCGCGAG 996
QY      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB      995 GCTGCTTCATCCACTGCCCGACGAGAACGAGCAGACTGGCCCGAGGTTCCTTCTGCG 936
QY      61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB      935 TTCAAGAGAGCTGGAGGCTGGAGCCGATGACGACCCCATAGAGAACATAAAGCAT 876
QY      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB      875 TCGCCCGCTTGGCTTCTTCTGTCAGAACAGATTGAAGATTAACTTGTGTGA 816
QY      101 PheLeuLysLeuAspArgIleArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB      815 TTTTGAACCTGGACAGAGAAAGGCCAAGAACAAATTGCCAAGAGAAACCAATTAAG 756
QY      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 139
DB      755 AAGAAAGATTGTGAGAACTGGCGAAGAAAGTGGCGCTGCCATCGAGCGCTGGCC 699

RESULT 6
US-08-189-309B-1/c
; Sequence 1, Application US/08189309B
; Patent No. 6238875
; GENERAL INFORMATION:
; APPLICANT: Altieri, Darío C.
; TITLE OF INVENTION: Diagnostic Methods Useful in the Characterization of
; TITLE OF INVENTION: Lymphoproliferative Disease Characterized by Increased EPR-1
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10550 No. 6238875th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,309B
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/986,897
; FILING DATE: 10-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,957
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: 233.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 37..1047
; US-08-189-309B-1

Alignment Scores:
Pred. No.: 8.7e-104
Score: 107.00
Percent Similarity: 99.28%
Best Local Similarity: 99.28%
Query Match: 75.35%
DB: 3

US-09-690-825-34 (1-142) x US-08-189-309B-1 (1-1165)

QY      1 MetGlyAlaProThrIleuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB      1114 ATGGGTCCCGCCGAGCTTGGCCCTGCTGCGAGCCCTTTTCTCAAGAACACCCGATCTCT 1055
QY      21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB      1054 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCC-TCGACCCCGAGCGATGCGCGAG 996
QY      41 AlaGlyPheIleHisCysProThrGluAsnGluProAspAspProIleGluGluHisLysLysHis 80
DB      995 GCTGCTTCATCCACTGCCCGACGAGAACGAGCAGACTGGCCCGAGGTTCCTTCTGCG 936
QY      61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB      935 TTCAAGAGAGCTGGAGGCTGGAGCCGATGACGACCCCATAGAGAACATAAAGCAT 876
QY      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB      875 TCGCCCGCTTGGCTTCTTCTGTCAGAACAGATTGAAGATTAACTTGTGTGA 816
QY      101 PheLeuLysLeuAspArgIleArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB      815 TTTTGAACCTGGACAGAGAAAGGCCAAGAACAAATTGCCAAGAGAAACCAATTAAG 756
QY      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 139
DB      755 AAGAAAGATTGTGAGAACTGGCGAAGAAAGTGGCGCTGCCATCGAGCGCTGGCC 699

RESULT 7
US-09-016-434-918
; Sequence 918, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen U.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 918:
SEQUENCE CHARACTERISTICS:
LENGTH: 740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITV01
CLONE: 752848
US-09-016-434-918

Alignment Scores:
Pred. No.: 3,41e-89 Length: 740
Score: 93.00 Matches: 130
Percent Similarity: 98.48% Conservative: 0
Best Local Similarity: 98.48% Mismatches: 1
Query Match: 65.49% Indels: 2
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-016-434-918 (1-740)

QY 12 ProPheLeuLysAspHisArgIleSerThrPheLysAsnTrpProPheLeuGluGlyCys 31
DB 51 CCTTTCTCAAGAGACCCGACCTCTACATTCAGAACTGGCCCTTCTTGAGGGCTGC 110

QY 32 AlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGlu-AsnG 51
DB 111 GCCTGCACCCCGAGGGAGGCGCGGCTGCTTATCAGTCCCACTGA-NACGA 169

QY 51 uPcraPheLysAlaGluCysPhePheCysPheLysGluLeuGluGlyTyrGluProAspAs 71
DB 170 GCCAGACTTGCCCAAGTGTCTTCTGCTTCAAGAGCTGGAAGGCTGGAGCCAGATA 225

QY 71 PaapProIleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLys 91
DB 230 CGACCCCATAGAGAAACATTAAGCATTCGTCGGTGGCTTCTTCTGTCAGAA 289

QY 91 sGlnPheGluGluLeuThrLeuGluGluPheLeuLysAspArgIleAlaGlyAlaLysAs 111
DB 290 GCGATTGAAAGATTAACTTGTGTGATTTTGAACCTGAGACAGAAAGAGCCAGAA 349

QY 111 nLysIleAlaLysGluThrAsnAsnLysLysLysGluPheGluGluThrAlaLysLysVa 131
DB 350 CAAATATGCAAGAGAAACCAACAATAAGAGAAAGATTGAGAGAACTGCCAGAAAG 409

QY 131 lArGArgAlaIleGluGluLeuAlaAlaMetAsp 142
DB 410 GCGCCGTGCATGAGCAGCTGCTGCCATGAT 443

RESULT 8
US-09-513-999C-2315
Sequence 2315 Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2315
LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 52..399
FEATURE:
NAME/KEY: misc_feature
LOCATION: 32
OTHER INFORMATION: k=g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 279
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 280
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 318
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 342
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: UNSURE
LOCATION: 77
OTHER INFORMATION: Xaa=Asp or His
US-09-513-999C-2315

Alignment Scores:
Pred. No.: 1.68e-71 Length: 399
Score: 76.00 Matches: 115
Percent Similarity: 98.29% Conservative: 0
Best Local Similarity: 98.29% Mismatches: 1
Query Match: 53.52% Indels: 2
DB: 4 Gaps: 0

US-09-690-825-34 (1-142) x US-09-513-999C-2315 (1-399)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 52 ATGGGTGCCCGAGAGTTCCTCCCTGCGCAGCCCTTTCAGAGACCAACGCACTCT 111

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 112 ACATTCAGAAAGACTGGCCCTTCTTGAGGGCTGCGCTGACCCCGAGCGGAGCGAG 171

QY 41 AlaGlyPheIleHisCysPProThrGluGluGluProAspLeuAlaGluCysPhePheCys 60
DB 172 GCTGCTTCATCCACTGCCCCCACTGAGACAGACGACGACTTGCCCACTGTTCTTGC 231

QY 61 PheLysGluLeuGluGlyTyrGluProAspAspProIleGluGluHis-LysLysHis 80
DB 232 TTCAGAGAGCTGAGAGGCTGGAGGACAGATGACGACCCCATAGAGAGASA-TAAGAA 290

QY 80 sSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyG 100
DB 291 TTCGTCGGCTTGCGCTTCTTCTTCTGTAAGAGAGATTAAAGCTTGGTGA 350

QY 100 uPheLeuLysLeuAspArgIleAlaLysAlaLysAlaLysGlu 116
DB 351 ATTTTGAAGACTGACAGAGAAAGAGCAAGCAAAATTGCCAAGAA 399

RESULT 9
US-09-496-694B-10
Sequence 10 Application US/09496694B

Patent No. 6335194
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric E. Swazey
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/266,407
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 10
LENGTH: 955
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (109)...(531)
US-09-496-694B-10

Alignment Scores:
Pred. No.: 3,32e-34 Length: 955
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.87% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-10 (1-955)

QY 31 CysAlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysPProThrGluAsn 50
Db 199 TGCCCTCGGACCCCGAGCGCATGCGAGGCTGGCTTCATCCACTGCTACCGGAGAAC 258

QY 51 GluProAspPheAlaGlnCysPhePheCysPheAlaGlnGluGlyTTPGluProAsp 70
Db 259 GAGCTGATTTGGCCCGACGTTGTTTCTGCTTTAAGAAATTGGAGAGCTGGGAAACCGGAT 318

QY 71 Asp 71
Db 319 GAC 321

RESULT 10
US-08-975-080-35
Sequence 35, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-975-080-35

Alignment Scores:
Pred. No.: 5.48e-31 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x US-08-975-080-35 (1-14796)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
Db 5159 GAGGAACATAAAGACATTCCTCCGCTTCCCTTCTGCAAGAACCACTTGAA 5218

QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgLysAlaValAsnLysIle 113
Db 5219 GAATTAACCTTGGTGAATTTTGAACCTGACAGAAAGCCAGCAACCAATT 5275

RESULT 11
US-09-630-706-10
Sequence 10, Application US/09630706
Patent No. 6277640
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
FILE REFERENCE: RTS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 10
LENGTH: 14796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
NAME/KEY: CDS
LOCATION: (5158)...(5275)
NAME/KEY: CDS
LOCATION: (11955)...(12044)
US-09-630-706-10

Alignment Scores:
Pred. No.: 5.48e-31 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.46% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x US-09-630-706-10 (1-14796)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94
|||||

Db 5159 GAGGAAACATATAAAGCATTCGTCGGCTTCCTTCCTTCGTCAGAGAGCATTTGAA 5218
Qy 95 GtuleuThrlenglyGluPheleuLysLeuAspArgGluArgAlaLysAsnLysile 113
Db 5219 GAATTACCTTGCTGTAATTTTGGAAACTGGACAGAAAGGCCAAGACAAATTT 5275
RESULT 12
US-09-496-694B-3
; Sequence 3, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1998-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811) ... (2921)
; NAME/KEY: CDS
; LOCATION: (3174) ... (3283)
; NAME/KEY: CDS
; LOCATION: (5158) ... (5275)
; NAME/KEY: CDS
; LOCATION: (11955) ... (12044)
US-09-496-694B-3
Alignment Scores:
Pred. No.: 5,48e-31 Length: 14796
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27,46% Indels: 0
Gaps: 0
DB: 3
US-09-690-825-34 (1-142) x US-09-496-694B-3 (1-14796)
Qy 75 GtGluThrlenglyLysLysSerSerglyCysAlaPheleuSerValLysLysGlnPheGlu 94
Db 5159 GAGGAAACATATAAAGCATTCGTCGGCTTCCTTCCTTCGTCAGAGAGCATTTGAA 5218
Qy 95 GtuleuThrlenglyGluPheleuLysLeuAspArgGluArgAlaLysAsnLysile 113
Db 5219 GAATTACCTTGCTGTAATTTTGGAAACTGGACAGAAAGGCCAAGACAAATTT 5275
RESULT 13
US-09-283-144-1
; Sequence 1, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; TITLE OF INVENTION: between Survivin and Tubulin
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880.

; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: US 60/031,435
; EARLIER FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: DNA sequence of proximal 5' flanking region of
; OTHER INFORMATION: Survivin gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (291) .. (401)
US-09-283-144-1
Alignment Scores:
Pred. No.: 2,56e-30 Length: 417
Score: 37.00 Matches: 37
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26,06% Indels: 0
Gaps: 0
DB: 3
US-09-690-825-34 (1-142) x US-09-283-144-1 (1-417)
Qy 1 MetGlyAlaProThrLeuProProAlaTyrGlnProPheleuLysAspHisArgIleSer 20
Db 291 ATGGGTGCCCGAGGTTGCCCCCTGCTGCGAGCCCTTTCTCAAGAGACCGCATCTCT 350
Qy 21 ThrPheLysAsnTyrProPheleuGlnGlyCysAlaCysThrProGluArg 37
Db 351 ACATTCAAGAACTGGCCCTTCTTGAGGGGCTGGCGCTGACCCCGGAGCGG 401
RESULT 14
US-09-672-717-199
; Sequence 199, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-09-672-717-199
Alignment Scores:
Pred. No.: 0,079 Length: 30
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6,34% Indels: 0
Gaps: 0
DB: 4
US-09-690-825-34 (1-142) x US-09-672-717-199 (1-30)
Qy 69 ProAspAspProIleGluGluHis 77
Db 3 CCGATGAGACCCCATAGAGAAACAT 29

RESULT 15
US-09-496-694B-13
; Sequence 13, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-496-694B-13

Alignment Scores:
Pred. No.: 0.786
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.63%
DB: 3
Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-13 (1-26)

OY 62 LysGluLeuGluGlyTyrGluPro 69
|||
Db 2 AAGCAATTGGAGAGGCTGGGAACCC 25

Search completed: November 1, 2004, 20:33:50
Job time : 97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 1, 2004, 19:10:41 ; Search time 369 Seconds

(without alignments)
1973.223 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 778
Sequence: 1 MCAPPLPPAMOPFLMDHRIS.....EFETAKVRAISQLAAMD 142

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3413475 segs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlp
-O/cgnt2_1/USPTO.spool/p/US09690825/rnatc.0112004.105431.1918/app.query.fasta.1.327
-DB=Published Applications NA -QEXT=fastap -SUFFIX=trmpb -MIMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=DCT -THR MAX=100
-THR_MIN=0 -ALIGN=15 -NODE=LOCAL -OUTFMT=pcio -NORM=ext -HEARSTAE=500 -MIMLEN=0
-MAXLEN=2000000000 -USER=US09690825.@CGN.1.1.723.@rnatc.0112004.105431.1918
-NCPU=6 -ICPU=3 -NO MAP -LARGEDUERY -NEG SCORES=0 -WAIT -DSPELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WASN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications NA:*

- 1: /cgnt2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgnt2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgnt2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgnt2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 5: /cgnt2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgnt2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgnt2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgnt2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgnt2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgnt2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgnt2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgnt2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgnt2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgnt2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgnt2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgnt2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgnt2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgnt2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgnt2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgnt2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgnt2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	429	17	US-10-665-975-1
2	778	100.0	1619	9	US-09-918-186A-97
3	778	100.0	1619	15	US-10-181-315-97
4	778	100.0	1619	15	US-10-172-118-566
5	778	100.0	1619	15	US-10-388-360-324
6	778	100.0	1619	15	US-10-342-887-566
7	778	100.0	1619	17	US-10-283-975A-445
8	778	100.0	1619	17	US-10-657-022-99
9	778	100.0	1643	18	US-10-807-897-1
10	778	100.0	2404	13	US-10-071-766-109
11	778	100.0	2404	15	US-10-084-811-285
12	772	99.2	2570	17	US-10-741-601-210
13	772	99.2	2585	17	US-10-741-601-215
14	750.5	96.5	2639	17	US-10-741-601-215
15	750.5	96.5	2654	17	US-10-741-601-211
16	721	92.7	740	16	US-10-305-720-918
17	660	84.8	955	9	US-09-918-186A-10
18	660	84.8	955	15	US-10-181-316-10
19	660	84.8	955	18	US-10-807-897-3
20	638	82.0	578	17	US-10-741-601-213
21	525.5	67.5	2452	17	US-10-741-601-212
22	525.5	67.5	2467	17	US-10-741-601-214
23	382	49.1	14795	15	US-10-181-316-3
24	382	49.1	14796	9	US-09-954-456-1636
25	382	49.1	14796	9	US-09-954-456-1636
26	382	49.1	14796	9	US-09-954-456-1636
27	382	49.1	14796	9	US-09-954-456-1636
28	382	49.1	14796	9	US-09-954-456-1636
29	382	49.1	14796	9	US-09-954-456-1636
30	382	49.1	14796	9	US-09-954-456-1636
31	382	49.1	14796	9	US-09-954-456-1636
32	347	44.6	332	9	US-09-833-381-1331
33	298	38.3	555	15	US-10-029-386-9972
34	223	28.7	121	15	US-10-179-730-33
35	223	28.7	201	17	US-10-741-601-4404
36	223	28.7	201	17	US-10-741-601-4415
37	223	28.7	201	17	US-10-741-601-4451
38	223	28.7	201	17	US-10-741-601-4451
39	216	27.8	120	15	US-10-029-386-23672
40	216	27.8	120	15	US-10-029-386-23672
41	211	27.1	378	17	US-10-430-201-2114
42	211	27.1	378	17	US-10-430-201-2115
43	201.5	25.9	201	17	US-10-741-601-4427
44	201.5	25.9	201	17	US-10-741-601-4439
45	155	19.9	5502	16	US-10-641-643-1459

ALIGNMENTS

RESULT 1
US-10-665-975-1
Sequence 1, Application US/10665975
Publication No. US2004038119A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING
TITLE OF INVENTION: PROTEIN (HEXIP) IN MODULATION OF APOPTOSIS
FILE REFERENCE: BURNHAM.005A
CURRENT APPLICATION NUMBER: US/10/665,975
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/412,109
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 429
TYPE: DNA
ORGANISM: Homo sapiens
US-10-665-975-1

Alignment Scores:

Pred. No.: 1.7e-93 Length: 429
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-665-975-1 (1-429)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 1 ATGGAGTGGCCCGAGCTGAGCTGCTGCTGAGCCCTTTCTCAAGAGCCACCGCATCTCT 60
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 61 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCGCCCTGACCCCGGAGCGGATGGCCGAG 120
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 121 GCTGCTTCATCCACTGCTCCCACTGAGACGAGCCACACTTGGCCCACTTTCTTCTCTGC 180
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80
 DB 181 TTCAAGAGAGCTGGAGAGCTGGAGCCAGATGACGACCCCATAGAGGACATATAAAGCAT 240
 QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGluGlu 100
 DB 241 TCGTCCGCTTGGCTTCTTCTTCTGTCAGAGAGCATTTTAAAGATTAACTTGTGTGAA 300
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 DB 301 TTTTGAACCTGGACAGAGAAAGAGCCAGCAACAAATTGCAAGGAAACCAATTAAG 360
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
 DB 361 AAGAAAGATTGAGGAACTGCGAAGAAAGTGGCGCTGCCATCGAGAGCTGGCTGCC 420
 QY 141 MetAsp 142
 DB 421 ATGGAT 426

RESULT 2

US-09-918-186A-97
 ; Sequence 97, Application US/09918186A
 ; Patent No. US20020137708A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Elizabeth J. Ackermann
 ; APPLICANT: Eric E. Swayze
 ; APPLICANT: Lex M. Cowse
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
 ; FILE REFERENCE: ISPH-0585
 ; CURRENT APPLICATION NUMBER: US/09/918,186A
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 09/496,694
 ; PRIOR FILING DATE: 2000-02-02
 ; PRIOR APPLICATION NUMBER: 09/286,407
 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 09/163,162
 ; PRIOR FILING DATE: 1998-09-29
 ; NUMBER OF SEQ ID NOS: 250
 ; SEQ ID NO 97
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-918-186A-97

Alignment Scores:

Pred. No.: 1.04e-92 Length: 1619
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-186A-97 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
 DB 50 ATGGAGTGGCCCGAGCTGAGCTGCTGCTGAGCCCTTTCTCAAGAGCCACCGCATCTCT 109
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
 DB 110 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCGCCCTGACCCCGGAGCGGATGGCCGAG 169
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
 DB 170 GCTGCTTCATCCACTGCTCCCACTGAGACGAGCCAGCTTGGCCCACTTCTTCTCTGC 229
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80
 DB 230 TTCAAGAGAGCTGGAGAGCTGGAGCCAGATGACGACCCCATAGAGGACATATAAAGCAT 285
 QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGluGlu 100
 DB 230 TCGTCCGCTTGGCTTCTTCTTCTGTCAGAGAGCATTTTAAAGATTAACTTGTGTGAA 349
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
 DB 350 TTTTGAACCTGGACAGAGAAAGAGCCAGCAACAAATTGCAAGGAAACCAATTAAG 409
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140
 DB 410 AAGAAAGATTGAGGAACTGCGAAGAAAGTGGCGCTGCCATCGAGAGCTGGCTGCC 469
 QY 141 MetAsp 142
 DB 470 ATGGAT 475

RESULT 3

US-10-181-316-97
 ; Sequence 97, Application US/10181316
 ; Publication No. US200303211607A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Elizabeth J. Ackermann
 ; APPLICANT: Eric E. Swayze
 ; APPLICANT: Lex M. Cowse
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
 ; FILE REFERENCE: ISPH-0650
 ; CURRENT APPLICATION NUMBER: US/10/181,316
 ; PRIOR FILING DATE: 2002-07-16
 ; PRIOR APPLICATION NUMBER: PCT/US01/02939
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 09/496,694
 ; PRIOR FILING DATE: 2000-02-02
 ; PRIOR APPLICATION NUMBER: 09/286,407
 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 09/163,162
 ; PRIOR FILING DATE: 1998-09-29
 ; NUMBER OF SEQ ID NOS: 249
 ; SEQ ID NO 97
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-181-316-97

Alignment Scores:

Pred. No.: 1.04e-92 Length: 1619
 Score: 778.00 Matches: 142
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-97 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuYsAspHisArgIleSer 20
Db 50 ATGGGAGCCCCGACGTTGGCCCTTCTGCGACGCCCTTTCTCAAGACCAACCGCATCTCT 109
QY 21 ThrPheYsAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATTCACACGCCCCCTGAGAACGACCACTGGCCCAAGTGTTCCTTCTG 229
QY 61 PheYsGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIleYsIleHis 80
Db 230 TTCAAGAGCTGGAAAGCTGGGAGCGAGTGAAGACCCCATGAGGAACATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValIleYsGluPheGluGluLeuThrLeuGluGlu 100
Db 290 TCGTCCGCTTGGCGCTTCTTCTTCTGCAAGACGACTTGAAGATTAACTTGTGTA 349
QY 101 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnYs 120
Db 350 TTTTGAAACTGGACACAGAAAGAGCCAAATAATGCAAGGAAACCAACATTAAG 409
QY 121 YsYsGluPheGluGluThrAlaYsValArgArgAlaIleGluGluLeuAla 140
Db 410 AAGAAAGAAATTGAGGAAAGCTGGAAAGAGTGGCGGTCATGAGCACTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 4
US-10-172-118-566
; Sequence 566, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernarde, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2659
; SEQ ID NO 566
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001168
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-566

Alignment Scores:
Pred. No.: 1,04e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-172-118-566 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuYsAspHisArgIleSer 20
Db 50 ATGGGAGCCCCGACGTTGGCCCTTCTGCGACGCCCTTTCTCAAGACCAACCGCATCTCT 109
QY 21 ThrPheYsAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATTCACACGCCCCCTGAGAACGACCACTGGCCCAAGTGTTCCTTCTG 229
QY 61 PheYsGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIleYsIleHis 80
Db 230 TTCAAGAGCTGGAAAGCTGGGAGCGAGTGAAGACCCCATGAGGAACATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValIleYsGluPheGluGluLeuThrLeuGluGlu 100
Db 290 TCGTCCGCTTGGCGCTTCTTCTTCTGCAAGACGACTTGAAGATTAACTTGTGTA 349
QY 101 PheLeuYsLeuAspArgGluArgAlaYsAsnYsIleAlaYsGluThrAsnYs 120
Db 350 TTTTGAAACTGGACACAGAAAGAGCCAAATAATGCAAGGAAACCAACATTAAG 409
QY 121 YsYsGluPheGluGluThrAlaYsValArgArgAlaIleGluGluLeuAla 140
Db 410 AAGAAAGAAATTGAGGAAAGCTGGAAAGAGTGGCGGTCATGAGCACTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 5
US-10-388-360-324
; Sequence 324, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffie B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael, Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSTED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-324

Alignment Scores:
Pred. No.: 1,04e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-388-360-324 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuYsAspHisArgIleSer 20
Db 50 ATGGGAGCCCCGACGTTGGCCCTTCTGCGACGCCCTTTCTCAAGACCAACCGCATCTCT 109

QY 21 ThrpheylsAenTTPProPheleuGluGlyCysAlaCysThrProGluarMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169
QY 41 AlaglyheilleHsCysProThrGluasnGluProbspleuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTCCACAGAGACGACGACCTTGCGCCAGTGTCTTCTGCG 229
QY 61 PheylsGluLeuGluGlyTTPGluProAspAspProIleGluGluHsIlySlySHs 80
Db 230 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACTATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValIlySlyGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGGCTTCTTCTTCTGTCAGAGAGAGATTGAAGATTAAACCTTGCTGAA 349
QY 101 PheLeuIlyLeuAspAPAGGluArGAlaIlyAsnIlyIleAlaIlySgluThrAsnAllys 120
Db 350 TTTTGAACCTGCACAGAGAAAGCCAGAACAAATTGCMAAGAAACCAACAACTAAG 409
QY 121 LysIlySgluPheGluGluThrAlaIlySlyValIlyArgAlaIleGluGluLeuAlaIa 140
Db 410 AAGAAAGATTGTGAGAAAGCTGCGAAGAAAGTGGCGCTGCATCGACGAGCTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGCAT 475

RESULT 5

US-10-342-887-566
Sequence 566, Application US/10342887
Publication No. US20040058340A1
GENERAL INFORMATION:

APPLICANT: Dai, Hongyue
APPLICANT: He, Jindong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 566
LENGTH: 1619
TYPE: DNA
ORGANISM: Homo sapiens
US-10-342-887-566

Alignment Scores:

Pred. No.: 1,04e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-342-887-566 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaATPGLnProPheLeuIlyAspHisArgIleSer 20
Db 50 ATGGGTGCCCGAGCTGGCCCTGCTGCGACGCCCTTCTCAAGAGCACCGCATCTCT 109

QY 21 ThrpheylsAenTTPProPheleuGluGlyCysAlaCysThrProGluarMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169
QY 41 AlaglyheilleHsCysProThrGluasnGluProbspleuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCATCCACTGCCCTCCACAGAGACGACGACCTTGCGCCAGTGTCTTCTGCG 229
QY 61 PheylsGluLeuGluGlyTTPGluProAspAspProIleGluGluHsIlySlySHs 80
Db 230 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACTATAAAGCAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValIlySlyGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGGCTTCTTCTTCTGTCAGAGAGAGATTGAAGATTAAACCTTGCTGAA 349
QY 101 PheLeuIlyLeuAspAPAGGluArGAlaIlyAsnIlyIleAlaIlySgluThrAsnAllys 120
Db 350 TTTTGAACCTGCACAGAGAAAGCCAGAACAAATTGCMAAGAAACCAACAACTAAG 409
QY 121 LysIlySgluPheGluGluThrAlaIlySlyValIlyArgAlaIleGluGluLeuAlaIa 140
Db 410 AAGAAAGATTGTGAGAAAGCTGCGAAGAAAGTGGCGCTGCATCGACGAGCTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGCAT 475

RESULT 7

US-10-283-975A-445
Sequence 445, Application US/10283975A
Publication No. US20040110792A1
GENERAL INFORMATION:

APPLICANT: Ortho-Clinical Diagnostics, Inc.
TITLE OF INVENTION: Methods for Assessing and Treating Leukemia
FILE REFERENCE: CDS 293 PCT
CURRENT APPLICATION NUMBER: US/10/283,975A
CURRENT FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: 60/340,938
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/338,997
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/340,081
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/341,012
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 900
SOFTWARE: PatentIn version 3.1
SEQ ID NO 445
LENGTH: 1619
TYPE: DNA
ORGANISM: HUMAN
US-10-283-975A-445

Alignment Scores:

Pred. No.: 1,04e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-283-975A-445 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaATPGLnProPheLeuIlyAspHisArgIleSer 20
Db 50 ATGGGTGCCCGAGCTGGCCCTGCTGCGACGCCCTTCTCAAGAGCACCGCATCTCT 109
QY 21 ThrpheylsAenTTPProPheleuGluGlyCysAlaCysThrProGluarMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169
QY 41 AlaglyheilleHsCysProThrGluasnGluProAspLeuAlaGlnCysPhePheCys 60

```

Db      170 GGTGGTTATCCACGCCCCCTGAGAACGAGCAAGATGGTCCAGGTTCTTCTGTC
Qy      61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHISLysLysHIS
Db      230 TTCAGAGACTGGAGAGCTGGAGCCAGATGACGACCCCATAGAGAACATATAAGCAT
Qy      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu
Db      290 TCGTCGGGTGGCTTCTTCTTCTGTCAGAAAGCAAGTTGAAGAAATTAACTTGTGTA
Qy      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys
Db      350 TTTTAAACTGACAGAGAAAGCCAGAACAAATTGCAAGAGAACCAACATTAAG
Qy      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla
Db      410 AAGAAAGATTGAGAGAACTGGAGAGAAAGTCCGCTGACATCGAGCAGCTGCTGCC
Qy      141 MetAsp 142
Db      470 ATGGAT 475

RESULT 8
US-10-657-022-99
; Sequence 99, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPIPOPE SEQUENCES
; FILE REFERENCE: MANK, 032A
; CURRENT APPLICATION NUMBER: US/10/657, 022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-657-022-99

Alignment Scores:
Pred. No.:      1,046-92      Length:      1619
Score:          778.00      Matches:      142
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
Gaps:          17          Gaps:          0

US-09-690-825-34 (1-142) x US-10-657-022-99 (1-1619)
Qy      1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHISArgIleSer 20
Db      50 ATGGGTGCCCCGAGCTGGCCCCCTGCTGAGCGCTTCTTCAAGGACCCCATCTCT 109
Qy      21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      110 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCGCTGCACCCCGAGCGGATGGCCGAG 169
Qy      41 AlaGlyPheIleHISLysCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      170 GCTGCTTATCCACTGCCCCACAGACGAGCAACTGGGCCAGTGTCTTCTTCTGTC 229
Qy      61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHISLysLysHIS 80
Db      230 TTCAGAGACTGGAGAGCTGGAGCCAGATGACGACCCCATAGAGAACATATAAGCAT 289
Qy      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

```

```

Db      290 TCGTCGGGTGGCTTCTTCTTCTGTCAGAAAGCAAGTTGAAGAAATTAACTTGTGTA
Qy      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db      350 TTTTGAACCTGACAGAGAAAGCCAGAACAAATTGCAAGAGAACCAACATTAAG 409
Qy      121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla
Db      410 AAGAAAGATTGAGAGAACTGGAGAGAAAGTCCGCTGACATCGAGCAGCTGCTGCC 469
Qy      141 MetAsp 142
Db      470 ATGGAT 475

RESULT 9
US-10-807-897-1
; Sequence 1, Application US/10807897
; Publication No. US20040192631A1
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.
; TITLE OF INVENTION: The Scripts Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSRI-874.1
; CURRENT APPLICATION NUMBER: US/10/807, 897
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457, 009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-10-807-897-1

Alignment Scores:
Pred. No.:      1,066-92      Length:      1643
Score:          778.00      Matches:      142
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
Gaps:          18          Gaps:          0

US-09-690-825-34 (1-142) x US-10-807-897-1 (1-1643)
Qy      1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHISArgIleSer 20
Db      45 ATGGGTGCCCCGAGCTGGCCCCCTGCTGAGCGCTTCTTCAAGGACCCCATCTCT 104
Qy      21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db      105 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCGCTGCACCCCGAGCGGATGGCCGAG 164
Qy      41 AlaGlyPheIleHISLysCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db      165 GCTGCTTATCCACTGCCCCACAGACGAGCAACTGGGCCAGTGTCTTCTTCTGTC 224
Qy      61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHISLysLysHIS 80
Db      225 TTCAGAGACTGGAGAGCTGGAGCCAGATGACGACCCCATAGAGAACATATAAGCAT 284
Qy      81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db      285 TCGTCGGGTGGCTTCTTCTTCTGTCAGAAAGCAAGTTGAAGAAATTAACTTGTGTA 344
Qy      101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db      345 TTTTGAACCTGACAGAGAAAGCCAGAACAAATTGCAAGAGAACCAACATTAAG 404

```

QY 121 LysylsglupehgiugluThralAllysValargAlailegiuglnleuAla140
DB 405 AAGAAAGATTGTGAGAAAGTGCAGAAAGTGGCCGTGCATCGAGCGTGGCTGCC 464
QY 141 Metasp 142
DB 465 ATGGAT 470

RESULT 10
US-10-071-766-109
; Sequence 109, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Hwei-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO: 109
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inocyte ID No. US20020192678A1 251651.4
; NAME/KEY: unsure
; LOCATION: 710, 717, 724, 982-1007
; OTHER INFORMATION: a, t, c, g, or other
US-10-071-766-109

Alignment Scores:
Pred. No.: 1,78e-92 Length: 2404
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-071-766-109 (1-2404)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 56 ATGGGTGCCCCGAGCGTGGCCCCCTGGCCCTGTCAGAGGACCAACCGCATCTCT 115
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 116 ACATTCAAGAACTGGCCCTTCTGGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 175
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 176 GCTGGCTTCATCCACTGCCCACTGAGAACGAGCCAGACTTGGCCCAAGTCTTCTCTGC 235
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80
DB 236 TTCAAGAGCTGGAAGGCTGGAGCCGATGACGACCCCATAGAGAACTAAAGACAT 295
QY 81 SerSerGlyCysAlaPheLeuSerValIlyslsGlnPheGluGluLeuThrLeuGlyGlu 100
DB 296 TCGTCCGGTTGCGCTTCTTCTGTCAGAGACAGATTGAAGATTAAACCTTGGTGA 355
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 356 TTTTGGAACTGGGCAAGAAAGAGCCAGAACAAATTGCAAGAAACCAACATAG 415
QY 121 LysylsglupehgiugluThralAllysValargAlailegiuglnleuAla140
DB 416 AAGAAAGATTGTGAGAAAGTGCAGAAAGTGGCCGTGCATCGAGCGTGGCTGCC 475
QY 141 Metasp 142
DB 476 ATGGAT 481

RESULT 11
US-10-084-817-285
; Sequence 285, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO: 285
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inocyte ID No. US20030119009A1 251651.4
; NAME/KEY: unsure
; LOCATION: 710, 717, 724
; OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-285

Alignment Scores:
Pred. No.: 1,78e-92 Length: 2404
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-084-817-285 (1-2404)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 56 ATGGGTGCCCCGAGCGTGGCCCCCTGGCCCTGTCAGAGGACCAACCGCATCTCT 115
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 116 ACATTCAAGAACTGGCCCTTCTGGAGGGCTGGCCCTGCACCCCGAGCGGATGGCCGAG 175
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 176 GCTGGCTTCATCCACTGCCCACTGAGAACGAGCCAGACTTGGCCCAAGTCTTCTCTGC 235
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80
DB 236 TTCAAGAGCTGGAAGGCTGGAGCCGATGACGACCCCATAGAGAACTAAAGACAT 295
QY 81 SerSerGlyCysAlaPheLeuSerValIlyslsGlnPheGluGluLeuThrLeuGlyGlu 100
DB 296 TCGTCCGGTTGCGCTTCTTCTGTCAGAGACAGATTGAAGATTAAACCTTGGTGA 355
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 356 TTTTGGAACTGGGCAAGAAAGAGCCAGAACAAATTGCAAGAAACCAACATAG 415
QY 121 LysylsglupehgiugluThralAllysValargAlailegiuglnleuAla140
DB 416 AAGAAAGATTGTGAGAAAGTGCAGAAAGTGGCCGTGCATCGAGCGTGGCTGCC 475
QY 141 Metasp 142
DB 476 ATGGAT 481

RESULT 12


```
US-10-741-601-210
; Sequence 210, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-210

Alignment Scores:
Pred. No.: 1,226-91      Length: 2570
Score: 772.00           Matches: 141
Percent Similarity: 99.30%  Conservative: 0
Best Local Similarity: 99.30%  Mismatches: 1
Query Match: 99.23%      Indels: 0
DB: 17                  Gaps: 0

US-09-690-825-34 (1-142) x US-10-741-601-210 (1-2570)
QY 1 MetGlyAlaProThrLeuProProAlaTPrGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGACGCTTGCCCTGCTGCGACCCCTTCTCAAGACCAACCGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCGCTGCACCCCGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 195 GCGGCTTCATCCACTGCCCCCACTGAGAACGACGACTGGCCCCAGTGTCTTCTTGC 254
QY 61 PheLeuGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGAAATATAAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCGTCCGGTGGCCCTTCTTCTGTCAGAAAGCATTTGAAGAAATTAACCTGTGTGA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 375 TTTTGAACCTGACAGAGAAAGCCCAAGACAAATTCGAAAGAAACCAACATAAG 434
QY 121 LysLysGluPheGluGluGluThrAlaLysValArgArgAlaIleGluGluLeuAlaAla 140
DB 435 AAGAAGAAATTTGAGAGAACTGCGRAGAAAGTGGCGGTGCATCGAGCAGCTGGTGC 494
QY 141 MetAsp 142
DB 495 ATGGAT 500

RESULT 13
US-10-741-601-216
; Sequence 216, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-216
```

```
; SEQ ID NO 216
; LENGTH: 2585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-216

Alignment Scores:
Pred. No.: 1,236-91      Length: 2585
Score: 772.00           Matches: 141
Percent Similarity: 99.30%  Conservative: 0
Best Local Similarity: 99.30%  Mismatches: 1
Query Match: 99.23%      Indels: 0
DB: 17                  Gaps: 0

US-09-690-825-34 (1-142) x US-10-741-601-216 (1-2585)
QY 1 MetGlyAlaProThrLeuProProAlaTPrGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGACGCTTGCCCTGCTGCGACCCCTTCTCAAGACCAACCGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCGCTGCACCCCGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 195 GCGGCTTCATCCACTGCCCCCACTGAGAACGACGACTGGCCCCAGTGTCTTCTTGC 254
QY 61 PheLeuGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGAAATATAAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCGTCCGGTGGCTTCTTCTTCTGTCAGAAAGCATTTGAAGAAATTAACCTGTGTGA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
DB 375 TTTTGAACCTGACAGAGAAAGCCCAAGACAAATTCGAAAGAAACCAACATAAG 434
QY 121 LysLysGluPheGluGluGluThrAlaLysValArgArgAlaIleGluGluLeuAlaAla 140
DB 435 AAGAAGAAATTTGAGAGAACTGCGRAGAAAGTGGCGGTGCATCGAGCAGCTGGTGC 494
QY 141 MetAsp 142
DB 495 ATGGAT 500

RESULT 14
US-10-741-601-215
; Sequence 215, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 2639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-215

Alignment Scores:
Pred. No.: 8,96-89      Length: 2639
Score: 750.50           Matches: 141
Percent Similarity: 85.45%  Conservative: 0
Best Local Similarity: 85.45%  Mismatches: 1
Query Match: 96.47%      Indels: 23
```

DB: 17 Gaps: 1
US-09-690-825-34 (1-142) x US-10-741-601-215 (1-2639)
QY 1 MetGlyAlaProThrLeuProPheProAlaIleProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGAGCGTTGCCCCCTGCGCGAGCCCTTCTCAAGGACCAACCGCATCTT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCCCTTTGGAGGCTGCCCCCTGCACCCCGAGCGGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 195 GCTGGCTTCATCCACTGCGCCCACTGAGACGAGCCAGACTTGGCCCACTTTCTTCTGCG 254
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIle----- 74
DB 255 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACACCCCATTTGGCCGCGGACAGGTGGCT 314
QY 75 -----GluGluHis 77
DB 315 TACGCTGTAAATACAGACACTTTGGAGGCCGAGCGCGGATCAGAGAGAGAACT 374
QY 78 LysIlyHisSerSerGlyCysAlaPheLeuSerValIlyLysGluPheGluLeuThr 97
DB 375 AAAAAGCATTCGTCGCGTTGCGCTTCTTCTGTCAAGAGCAGATTGAAGATTAAACC 434
QY 98 LeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnIlyIleAlaLysGluThr 117
DB 435 CTGGTGAATTTTGAACCTGACAGAGAAAGCCCAAGAACAAATTGCAAGAGAAACC 494
QY 118 AsnAsnIlyLysLysGluPheGluGluThrAlaLysLysValaArgArgAlaIleGluGln 137
DB 495 AACAAATAGAGAAAGAAATTGAGAGAACTGCGRAGAAAGTGGCGGTCATCGAGCAG 554
QY 138 LeuAlaAlaMetAsp 142
DB 555 CTGGCTGCCATGAT 569
RESULT 15
US-10-741-601-211
; Sequence 211, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILU, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741.601
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 2654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-211
Alignment Scores:
Pred. No.: 8,976-89 Length: 2654
Score: 750.50 Matches: 141
Percent Similarity: 85.45% Conservative: 0
Best Local Similarity: 85.45% Mismatches: 1
Query Match: 96.47% Indels: 23
DB: 17 Gaps: 1
US-09-690-825-34 (1-142) x US-10-741-601-211 (1-2654)
QY 1 MetGlyAlaProThrLeuProPheProAlaIleProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCCGAGCGTTGCCCCCTGCGCGAGCCCTTCTCAAGGACCAACCGCATCTT 134

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCCCTTCTTGGAGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
DB 195 GCTGGCTTCATCCACTGCGCCCACTGAGACGAGCCAGACTTGGCCCACTTTCTTCTGCG 254
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIle----- 74
DB 255 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACACCCCATTTGGCCGCGGACAGGTGGCT 314
QY 75 -----GluGluHis 77
DB 315 TACGCTGTAAATACAGACACTTTGGAGGCCGAGCGCGGATCAGAGAGAGAACT 374
QY 78 LysIlyHisSerSerGlyCysAlaPheLeuSerValIlyLysGluPheGluLeuThr 97
DB 375 AAAAAGCATTCGTCGCGTTGCGCTTCTTCTGTCAAGAGCAGATTGAAGATTAAACC 434
QY 98 LeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnIlyIleAlaLysGluThr 117
DB 435 CTGGTGAATTTTGAACCTGACAGAGAAAGCCCAAGAACAAATTGCAAGAGAAACC 494
QY 118 AsnAsnIlyLysLysGluPheGluGluThrAlaLysLysValaArgArgAlaIleGluGln 137
DB 495 AACAAATAGAGAAAGAAATTGAGAGAACTGCGRAGAAAGTGGCGGTCATCGAGCAG 554
QY 138 LeuAlaAlaMetAsp 142
DB 555 CTGGCTGCCATGAT 569

Search completed: November 1, 2004, 20:32:08
Job time : 376 secs